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Docket No: 4305/1E144-1/S1

Date: March 16, 1999

Hon. Commissioner of
Patents and Trademarks
Washington, DC 20231

Sir:

Enclosed please find an application for United States patent as identified below:

Inventor/s (name ALL inventors): Hans Henrik IPSEN, Michael Dho Spangfort and
Jorgen Nedergaard LARSEN

Title: NOVEL RECOMBINANT ALLERGENS

including the items indicated:

1. Specification and 42 claims: 1 indep.; 41 dep.
2. ☒ Declaration and power of attorney [Unsigned]
3. ☒ Formal drawings, 14 sheets (Figs. 1-14)
☐ Informal drawings, _ sheets (Figs.)
4. ☐ Assignment for recording to:
5. ☐ Verified Statement Claiming Small Entity Status
6. ☐ Check in amount of \$.00, (\$ filing; \$ recording; \$ surcharge)
(See attached Fee Computation Sheet)

jc551 U.S. PTO
09/270910

03/16/99

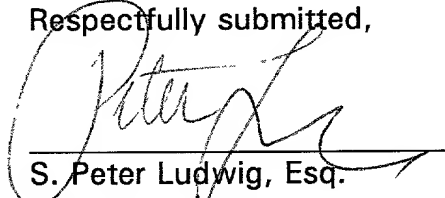
7. ☒ Preliminary Amendment.
8. ☒ Please amend the description by inserting the following paragraph after the line containing the title on page 1:
"This patent application claims the priority of U.S. provisional patent application No. 60/078,371, which is incorporated herein by reference."

Priority is claimed for this application, corresponding application/s having been filed as follows:

Country:	United States of America
Number:	60/078,371
Date:	March 18, 1998

The priority documents ☒ are on record as above
☐ will follow.

Respectfully submitted,


S. Peter Ludwig, Esq.
Reg. No. 25,351
Attorney for Applicant(s)

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J. JOSEPH J. JOSEPH
Name (Print) Signature

File No: 4305/1E144-US1

IN THE UNITED STATES PATENT AND TRADEMARK OFFICE

In re Application of:

HANS HENRIK IPSEN, et al.

Serial No : Unassigned
Filed : Concurrently Herewith
For : NOVEL RECOMBINANT ALLERGENS

PRELIMINARY AMENDMENT

Hon. Commissioner of
Patents and Trademarks
Washington, DC 20231

Sir:

Prior to examining the above-identified patent application please enter
the following amendment:

IN THE CLAIMS:

Claim 3, line 1, delete "or 2" ;

Claim 4, line 1, delete "claims 1-3" and insert - - claim 1 - -;

Claim 6, lines 1-2, delete "claims 2-5" and insert - - claim 2 - -;

Claim 8, lines 1-2, delete "claims 2-7" and insert -- claim 2 - -;

Claim 9, lines 1-2, delete "claims 2-5" and insert - - claim 2 - -;

Claim 10, lines 1-2, delete "claims 1-9" and insert - - claim 1 - -;

Claim 23, lines 1-2, delete "claims 1-9" and insert - - claim 1 - -;

Claim 26, lines 1-2, delete "claims 23-25" and insert - - claim 23 - -;

Claim 27, lines 1-2, delete "claims 23-26" and insert - - claim 26 - -;

Claim 28, lines 1-2, delete "claims 25-27" and insert - - claim 25 - -;

Claim 29, line 2, delete "any one of claims 1-29" and insert - - claim 1 - -;

Claim 31, line 1, delete "or 30";

Claim 32, line 1, delete "claims 1-28" and insert - - claim 1 - -;

Claim 33, line 3, delete "claims 1-28" and insert - - claim 1 - -;

Delete claims 35 - 39 and insert new claims 40 to 47 as follows:

- - 40. Method of generating an immune response in a subject comprising administering to the subject at least one recombinant allergen according to claim 1. -

- - 41. Method of generating an immune response in a subject by administering a pharmaceutical composition according to claim 33. - -

- - 42. Process for preparing a pharmaceutical composition according to claim 33 comprising mixing at least one recombinant allergen with pharmaceutically acceptable substances and/or excipients. - -

- - 43. Vaccination or treatment of a subject comprising administering to the subject at least one recombinant allergen according to claim 1. - -

- - 44. Vaccination or treatment of a subject comprising administering to the subject a pharmaceutical composition according to claim 33.- -

- - 45. Method for the treatment, prevention or alleviation of allergic reactions comprising administering to a subject a recombinant allergen according to claim 1. - -

- - 46. Method for the treatment, prevention or alleviation of allergic reactions comprising administering to a subject a pharmaceutical composition according to claim 33.- -


- - 47. Pharmaceutical composition obtainable by the process according to claim 36.

REMARKS

This amendment is made to eliminate multiple dependent claims and reduce the filing fee.

Early examination on the merits is respectfully solicited.

Respectfully submitted,

By: 
S. Peter Ludwig
Registration No. 25,351
Attorney for Applicant(s)

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Joseph H. Joseph
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NOVEL RECOMBINANT ALLERGENS

FIELD OF THE INVENTION

5 The present invention relates to novel recombinant
allergens, which are non-naturally occurring mutants
derived from naturally occurring allergens. Further, the
invention relates to a method of preparing such
recombinant allergens as well as to pharmaceutical
10 compositions, including vaccines, comprising the
recombinant allergens. In further embodiments, the
present invention relates to methods of generating immune
responses in a subject, vaccination or treatment of a
subject as well as processes for preparing the
15 compositions of the invention.

BACKGROUND OF THE INVENTION

20 Genetically predisposed individuals become sensitised
(allergic) to antigens originating from a variety of
environmental sources, to the allergens of which the
individuals are exposed. The allergic reaction occurs
when a previously sensitised individual is re-exposed to
the same or a homologous allergen. Allergic responses
25 range from hay fever, rhinoconductivitis, rhinitis and
asthma to systemic anaphylaxis and death in response to
e.g. bee or hornet sting or insect bite. The reaction is
immediate and can be caused by a variety of atopic
allergens such as compounds originating from grasses,
30 trees, weeds, insects, food, drugs, chemicals and
perfumes.

However, the responses do not occur when an individual is
exposed to an allergen for the first time. The initial
35 adaptive response takes time and does usually not cause
any symptoms. But when antibodies and T cells capable of

reacting with the allergen have been produced, any subsequent exposure may provoke symptoms. Thus, allergic responses demonstrate that the immune response itself can cause significant pathological states, which may be life threatening.

The antibodies involved in atopic allergy belong primarily to immunoglobulins of the IgE class. IgE binds to specific receptors on the surface of mast cells and basophils. Following complex formation of a specific allergen with IgE bound to mast cells, receptor cross-linking on the cell surface results in signalling through the receptors and the physiological response of the target cells. Degranulation results in the release of i.a. histamine, heparin, a chemotactic factor for eosinophilic leukocytes, leukotrienes C4, D4 and E4, which cause prolonged constriction of the bronchial smooth muscle cells. The resulting effects may be systemic or local in nature.

The antibody-mediated hypersensitivity reactions can be divided into four classes, namely type I, type II, type III and type IV. Type I allergic reactions is the classic immediate hypersensitivity reaction occurring within seconds or minutes following antigen exposure. These symptoms are mediated by allergen specific IgE.

Commonly, allergic reactions are observed as a response to protein allergens present e.g. in pollens, house dust mites, animal hair and dandruff, venoms, and food products.

In order to reduce or eliminate allergic reactions, carefully controlled and repeated administration of allergy vaccines is commonly used. Allergy vaccination is traditionally performed by parenteral, intranasal, or

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sublingual administration in increasing doses over a fairly long period of time, and results in desensitisation of the patient. The exact immunological mechanism is not known, but induced differences in the phenotype of allergen specific T cells is thought to be of particular importance.

Antibody-binding epitopes (B-cell epitopes)

X-ray crystallographic analyses of Fab-antigen complexes has increased the understanding of antibody-binding epitopes. According to this type of analysis antibody-binding epitopes can be defined as a section of the surface of the antigen comprising atoms from 15-25 amino acid residues, which are within a distance from the atoms of the antibody enabling direct interaction. The affinity of the antigen-antibody interaction can not be predicted from the enthalpy contributed by van der Waals interactions, hydrogen bonds or ionic bonds, alone. The entropy associated with the almost complete expulsion of water molecules from the interface represent an energy contribution similar in size. This means that perfect fit between the contours of the interacting molecules is a principal factor underlying antigen-antibody high affinity interactions.

Allergy vaccination

The concept of vaccination is based on two fundamental characteristics of the immune system, namely specificity and memory. Vaccination will prime the immune system of the recipient, and upon repeated exposure to similar proteins the immune system will be in a position to respond more rigorously to the challenge of for example a microbial infection. Vaccines are mixtures of proteins intended to be used in vaccination for the purpose of

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generating such a protective immune response in the recipient. The protection will comprise only components present in the vaccine and homologous antigens.

- 5 Compared to other types of vaccination allergy vaccination is complicated by the existence of an ongoing immune response in allergic patients. This immune response is characterised by the presence of allergen specific IgE mediating the release of allergic symptoms
10 upon exposure to allergens. Thus, allergy vaccination using allergens from natural sources has an inherent risk of side effects being in the utmost consequence life threatening to the patient.
- 15 Approaches to circumvent this problem may be divided in three categories. In practise measures from more than one category are often combined. First category of measures includes the administration of several small doses over prolonged time to reach a substantial accumulated dose.
- 20 Second category of measures includes physical modification of the allergens by incorporation of the allergens into gel substances such as aluminium hydroxide. Aluminium hydroxide formulation has an adjuvant effect and a depot effect of slow allergen
25 release reducing the tissue concentration of active allergen components. Third category of measures include chemical modification of the allergens for the purpose of reducing allergenicity, i.e. IgE binding.
- 30 The detailed mechanism behind successful allergy vaccination remains controversial. It is, however, agreed that T cells play a key role in the overall regulation of immune responses. According to current consensus the relation between two extremes of T cell phenotypes, Th1
35 and Th2, determine the allergic status of an individual. Upon stimulation with allergen Th1 cells secrete

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interleukines dominated by interferon- γ leading to protective immunity and the individual is healthy. Th2 cells on the other hand secrete predominantly interleukin 4 and 5 leading to IgE synthesis and eosinophilia and the individual is allergic. *In vitro* studies have indicated the possibility of altering the responses of allergen specific T cells by challenge with allergen derived peptides containing relevant T cell epitopes. Current approaches to new allergy vaccines are therefore largely based on addressing the T cells, the aim being to silence the T cells (anergy induction) or to shift the response from the Th2 phenotype to the Th1 phenotype.

In WO 97/30150 (ref. 1), a population of protein molecules is claimed, which protein molecules have a distribution of specific mutations in the amino acid sequence as compared to a parent protein. From the description, it appears that the invention is concerned with producing analogues which are modified as compared to the parent protein, but which are taken up, digested and presented to T cells in the same manner as the parent protein (naturally occurring allergens). Thereby, a modified T cell response is obtained. Libraries of modified proteins are prepared using a technique denoted PM (Parsimonious Mutagenesis).

In WO 92/02621 (ref. 2), recombinant DNA molecules are described, which molecules comprise a DNA coding for a polypeptide having at least one epitope of an allergen of trees of the order *Fagales*, the allergen being selected from *Aln g 1*, *Cor a 1* and *Bet v 1*. The recombinant molecules described herein do all have an amino acid sequence or part of an amino acid sequence that corresponds to the sequence of a naturally occurring allergen.

WO 90/11293 (ref. 3) relates i.a. to isolated allergenic peptides of ragweed pollen and to modified ragweed pollen peptides. The peptides disclosed therein have an amino acid sequence corresponding either to the sequence of the naturally occurring allergen or to naturally occurring isoforms thereof.

Chemical modification of allergens

- Several approaches to chemical modification of allergens have been taken. Approaches of the early seventies include chemical coupling of allergens to polymers, and chemical cross-linking of allergens using formaldehyde, etc., producing the so-called 'allergoids'. The rationale behind these approaches was random destruction of IgE binding epitopes by attachment of the chemical ligand thereby reducing IgE-binding while retaining immunogenicity by the increased molecular weight of the complexes. Inherent disadvantages of 'allergoid' production are linked to difficulties in controlling the process of chemical cross-linking and difficulties in analysis and standardisation of the resulting high molecular weight complexes. 'Allergoids' are currently in clinical use and due to the random destruction of IgE binding epitopes higher doses can be administered as compared to conventional vaccines, but the safety and efficacy parameters are not improved over use of conventional vaccines.
- More recent approaches to chemical modification of allergens aim at a total disruption of the tertiary structure of the allergen thus eliminating IgE binding assuming that the essential therapeutic target is the allergen specific T cell. Such vaccines contain allergen sequence derived synthetic peptides representing minimal T cells epitopes, longer peptides representing linked T

cells epitopes, longer allergen sequence derived synthetic peptides representing regions of immunodominant T cell epitopes, or allergen molecules cut in two halves by recombinant technique. Another approach based on this
 5 rationale has been the proposal of the use of "low IgE binding" recombinant isoforms. In recent years it has become clear that natural allergens are heterogeneous containing isoallergens and variants having up to approximately 25% of their amino acids substituted. Some
 10 recombinant isoallergens have been found to be less efficient in IgE binding possibly due to irreversible denaturation and hence total disruption of tertiary structure.

15 In vitro mutagenesis and allergy vaccination

Attempts to reduce allergenicity by *in vitro* site directed mutagenesis have been performed using several allergens including Der f 2 (Takai et al, ref. 4), Der p
 20 2 (Smith et al, ref. 5), a 39 kDa *Dermatophagoides farinae* allergen (Aki et al, ref. 6), bee venom phospholipase A2 (Förster et al, ref. 7), Ara h 1 (Burks et al, ref. 8), Ara h 2 (Stanley et al, ref. 9), Bet v 1 (Ferreira et al, ref. 10 and 11), birch profilin
 25 (Wiedemann et al, ref. 12), and Ory s 1 (Alvarez et al, ref. 13).

The rationale behind these approaches, again, is addressing allergen specific T cells while at the same
 30 time reducing the risk of IgE mediated side effects by reduction or elimination of IgE binding by disruption of the tertiary structure of the recombinant mutant allergen. The rationale behind these approaches does not include the concept of dominant IgE binding epitopes and
 35 it does not include the concept of initiating a new protective immune response which also involves B-cells

and antibody generation.

5 The article by Ferreira et al (ref. 11) describes the use
of site directed mutagenesis for the purpose of reducing
IgE binding. Although the three-dimensional structure of
Bet v 1 is mentioned in the article the authors do not
use the structure for prediction of surface exposed amino
acid residues for mutation, half of which have a low
degree of solvent exposure. Rather they use a method
10 developed for prediction of functional residues in
proteins different from the concept of structure based
identification of conserved surface areas described here.
Although the authors do discuss conservation of α -carbon
backbone tertiary structure this concept is not a part of
15 the therapeutic strategy but merely included to assess in
vitro IgE binding. Furthermore, the evidence presented is
not adequate since normalisation of CD-spectra prevents
the evaluation of denaturation of a proportion of the
sample, which is a common problem. The therapeutic
20 strategy described aim at inducing tolerance in allergen
specific T cells and initiation of a new immune response
is not mentioned.

25 The article by Wiedemann et al. (ref. 12) describes the
use of site directed mutagenesis and peptide synthesis
for the purpose of monoclonal antibody epitope
characterisation. The authors have knowledge of the
tertiary structure of the antigen and they use this
knowledge to select a surface exposed amino acid for
30 mutation. The algorithm used can be said to be opposite
to the one described by the present inventors since an
amino acid differing from homologous sequences is
selected. The study demonstrates that substitution of a
surface exposed amino acid has the capacity to modify the
35 binding characteristics of a monoclonal antibody, which
is not surprising considering common knowledge. The

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experiments described are not designed to assess modulation in the binding of polyclonal antibodies such as allergic patients' serum IgE. One of the experiments contained do apply serum IgE and although this experiment
5 is not suitable for quantitative assessment, IgE binding does not seem to be affected by the mutations performed.

The article by Smith et al. (ref. 5) describes the use of site directed mutagenesis for the purpose of monoclonal
10 antibody epitope mapping and reduction of IgE binding. The authors have no knowledge of the tertiary structure and make no attempt to assess the conservation of α -carbon backbone tertiary structure. The algorithm used
15 does not ensure that amino acids selected for mutation are actually exposed to the molecular surface. Only one of the mutants described lead to a substantial reduction in IgE binding. This mutant is deficient in binding of all antibodies tested indicating that the tertiary structure is disrupted. The authors do not define a
20 therapeutic strategy and initiation of a new immune response is not mentioned.

The article by Colombo et al. (ref. 14) describes the study of an IgE binding epitope by use of site directed
25 mutagenesis and peptide synthesis. The authors use a three dimensional computer model structure based on the crystal structure of a homologous protein to illustrate the presence of the epitope on the molecular surface. The further presence of an epitope on a different allergen
30 showing primary structure homology is addressed using synthetic peptides representing the epitope. The therapeutic strategy is based on treatment using this synthetic peptide representing a monovalent IgE binding epitope. Conserved surface areas between homologous
35 allergens as well as the therapeutic concept of initiating a new protective immune response are not

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mentioned.

The article by Spangfort et al. (ref. 15) describes the three-dimensional structure and conserved surface exposed patches of the major birch allergen. The article does not mention major IgE binding epitopes nor site directed mutagenesis, neither is therapeutic application addressed.

In none of the studies described above is IgE binding reduced by substitution of surface exposed amino acids while conserving α -carbon backbone tertiary structure. The rationale behind above-mentioned approaches does not include the concept of dominant IgE binding epitopes and it does not include the therapeutic concept of initiating a new protective immune response.

BRIEF DESCRIPTION OF THE FIGURES

Figure 1 shows mutant-specific oligonucleotide primers used for Bet v 1 mutant number 1. Mutated nucleotides are underlined.

Figure 2 shows two generally applicable primers (denoted "all-sense" and "all non-sense"), which were synthesised and used for all mutants.

Figure 3 shows an overview of all Bet v 1 mutations.

Figure 4 shows the inhibition of the binding of biotinylated recombinant Bet v 1 to serum IgE from a pool of allergic patients by non-biotinylated Bet v 1 and by Bet v 1 Glu45Ser mutant.

Figure 5 shows the inhibition of the binding of biotinylated recombinant Bet v 1 to serum IgE from a pool

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of allergic patients by non-biotinylated *Bet v 1* and by *Bet v 1* mutant Asn28Thr+Lys32Gln.

Figure 6 shows the inhibition of the binding of
5 biotinylated recombinant *Bet v 1* to serum IgE from a pool of allergic patients by non-biotinylated *Bet v 1* and by *Bet v 1* Pro108Gly mutant.

Figure 7 shows the inhibition of the binding of
10 biotinylated recombinant *Bet v 1* to serum IgE from a pool of allergic patients by non-biotinylated *Bet v 1* and by *Bet v 1* Glu60Ser mutant.

Figure 8 shows the CD spectra of recombinant and
15 Triple-patch mutant, recorded at close to equal concentrations.

Figure 9 shows the inhibition of the binding of
20 biotinylated recombinant *Bet v 1* to serum IgE from a pool of allergic patients by non-biotinylated *Bet v 1* and by *Bet v 1* Triple-patch mutant.

Figure 10 shows solvent accessibility of individually
25 aligned antigen 5 residues and alignment of *Vespula* antigen 5 sequences (left panel). On the right panel of Figure 10 is shown the molecular surface of antigen 5 with conserved areas among *Vespula* antigen 5:s.

Figure 11 shows the sequence of the primer corresponding
30 to the amino terminus of *Ves v 5* derived from the sense strand. The sequence of the downstream primer is derived from the non-sense strand.

Figure 12 shows two generally applicable primers (denoted
35 "all sense" and "all non-sense", which were synthesised and used for all mutants.

Figure 13 shows an overview of all Ves v 5 mutations.

Figure 14 shows the inhibition of the binding of
5 biotinylated recombinant Ves v 5 to serum IgE from a pool
of allergic patients by non-biotinylated Ves v 5 and by
Ves v 5 Lys72Ala mutant.

OBJECT OF THE INVENTION

10

Rationale behind the present invention

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The current invention is based on a unique rationale.
According to this rationale the mechanism of successful
15 allergy vaccination is not an alteration of the ongoing
Th2-type immune response, but rather a parallel
initiation of a new Th1-type immune response involving
tertiary epitope recognition by B-cells and antibody
formation. This model is supported by the observation
20 that levels of specific IgE are unaffected by successful
vaccination treatment, and that successful treatment is
often accompanied by a substantial rise in allergen
specific IgG4. In addition, studies of nasal biopsies
before and after allergen challenge do not show a
25 reduction in T cells with the Th2-like phenotype, but
rather an increase in Th1-like T cells are observed. When
the vaccine (or pharmaceutical compositions) is
administered through another route than the airways, it
is hypothesised, that the new Th1-like immune response
30 evolves in a location physically separated from the
ongoing Th2 response thereby enabling the two responses
to exist in parallel.

Another important aspect of the rationale behind the
35 current invention is the assertion of the existence of
dominant IgE binding epitopes. It is proposed that these

dominant IgE binding epitopes are constituted by tertiary structure dependent coherent surface areas large enough to accommodate antibody binding and conserved among isoallergens, variants, and/or homologous allergens from related species. The existence of cross-reactive IgE capable of binding similar epitopes on homologous allergens is supported by the clinical observation that allergic patients often react to several closely related species, e.g. alder, birch, and hazel, multiple grass species, or several species of the house dust mite genus *Dermatophagoides*. It is furthermore supported by laboratory experiments demonstrating IgE cross-reactivity between homologous allergens from related species and the capacity of one allergen to inhibit the binding of IgE to homologous allergens (Ipsen et al. 1992, ref. 16). It is well known that exposure and immune responses are related in a dose dependent fashion. Based on the combination of these observations it is hypothesised that conserved surface areas are exposed to the immune system in higher doses than non-conserved surface areas resulting in the generation of IgE antibodies with higher affinities, hence the term 'dominant IgE binding epitopes'.

According to this rationale it is essential that the allergen has an α -carbon backbone tertiary structure which essentially is the same as that of the natural allergen, thus ensuring conservation of the surface topology of areas surrounding conserved patches representing targets for mutagenesis aimed at reducing IgE binding. By fulfilling these criteria the allergen has the potential to be administered in relatively higher doses improving its efficacy in generating a protective immune response without compromising safety.

SUMMARY OF THE INVENTION

The present invention relates to the introduction of artificial amino acid substitutions into defined critical positions while retaining the α -carbon backbone tertiary structure of the allergen.

5

The invention provides a recombinant allergen, which is a non-naturally occurring mutant derived from a naturally occurring allergen, wherein at least one surface-exposed, conserved amino acid residue of a B cell epitope is substituted by another residue which does not occur in the same position in the amino acid sequence of any known homologous protein within the taxonomic order from which said naturally occurring allergen originates, said mutant allergen having essentially the same α -carbon backbone tertiary structure as said naturally occurring allergen, and the specific IgE binding to the mutated allergen being reduced as compared to the binding to said naturally occurring allergen.

20 Such recombinant allergen is obtainable by

a) identifying amino acid residues in a naturally occurring allergen which are conserved with more than 70% identity in all known homologous proteins within the taxonomic order from which said naturally occurring allergen originates;

b) defining at least one patch of conserved amino acid residues being coherently connected over at least 400 Å² of the surface of the three-dimensional of the allergen molecule as defined by having a solvent accessibility of at least 20%, said at least one patch comprising at least one B cell epitope; and

35 c) substituting at least one amino acid residue in said at least one patch by another amino acid being non-con-

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servative in the particular position while essentially preserving the overall α -carbon backbone tertiary structure of the allergen molecule.

- 5 Specific IgE binding to the mutated allergen is preferably reduced by at least 5%, preferably at least 10% in comparison to naturally-occurring isoallergens or similar recombinant proteins in an immuno assay with sera from source-specific IgE reactive allergic patients or
10 pools thereof.

Recombinant allergens according to the invention may suitably be derived from inhalation allergens originating i.a. from trees, grasses, herbs, fungi, house dust mites,
15 cockroaches and animal hair and dandruff. Important pollen allergens from trees, grasses and herbs are such originating from the taxonomic orders of *Fagales*, *Oleales* and *Pinales* including i.a. birch (*Betula*), alder (*Alnus*), hazel (*Corylus*), hornbeam (*Carpinus*) and olive (*Olea*),
20 the order of *Poales* including i.a. grasses of the genera *Lolium*, *Phelum*, *Poa*, *Cynodon*, *Dactylis* and *Secale*, the orders of *Asterales* and *Urticales* including i.a. herbs of the genera *Ambrosia* and *Artemisia*. Important inhalation allergens from fungi are i.a. such originating from the
25 genera *Alternaria* and *Cladosporium*. Other important inhalation allergens are those from house dust mites of the genus *Dermatophagoides*, those from cockroaches and those from mammals such as cat, dog and horse. Further, recombinant allergens according to the invention may be
30 derived from venom allergens including such originating from stinging or biting insects such as those from the taxonomic order of *Hymenoptera* including bees (superfamily *Apidae*), wasps (superfamily *Vespidea*), and ants (superfamily *Formicoidae*).

35

Specific allergen components include e.g. *Bet v 1* (B.

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verrucosa, birch), *Aln g 1* (*Alnus glutinosa*, alder), *Cor a 1* (*Corylus avelana*, hazel) and *Car b 1* (*Carpinus betulus*, hornbeam) of the *Fagales* order. Others are *Cry j 1* (*Pinales*), *Amb a 1* and 2, , *Art v 1* (*Asterales*), *Par j 1* (*Urticales*), *Ole e 1* (*Oleales*), *Ave e 1*, *Cyn d 1*, *Dac g 1*, *Fes p 1*, *Hol l 1*, *Lol p 1* and 5, *Pas n 1*, *Phl p 1* and 5, *Poa p 1*, 2 and 5, *Sec c 1* and 5, and *Sor h 1* (various grass pollens), *Alt a 1* and *Cla h 1* (fungi), *Der f 1* and 2, *Der p 1* and 2 (house dust mites, *D. farinae* and *D. pteronyssinus*, respectively), *Bla g 1* and 2, *Per a 1* (cockroaches, *Blatella germanica* and *Periplaneta americana*, respectively), *Fel d 1* (cat), *Can f 1* (dog), *Equ c 1*, 2 and 3 (horse), *Apis m 1* and 2 (honeybee), *Ves g 1*, 2 and 5, *Pol a 1*, 2 and 5 (all wasps) and *Sol i 1*, 2, 3 and 4 (fire ant).

In one embodiment, the recombinant allergen is derived from *Bet v 1*. Examples of substitutions are *Thr10Pro*, *Asp25Gly*, (*Asn28Thr + Lys32Gln*), *Glu45Ser*, *Asn47Ser*, *Lys55Asn*, *Thr77Ala*, *Pro108Gly* and (*Asn28Thr*, *Lys32Gln*, *Glu45Ser*, *Pro108Gly*. As apparent, the recombinant allergens may have one or more substitutions.

In another embodiment, the recombinant allergen is derived from a venom allergen from the taxonomic order of *Vespidae*, *Apidae* and *Formicoidae*.

In a further embodiment, the recombinant allergen is derived from *Ves v 5*. Examples of substitutions are *Lys72Ala* and *Tyr96Ala*. As apparent, the recombinant allergens may have one or more substitutions.

The present invention also provides a method of preparing a recombinant allergen as defined herein, comprising

a) identifying amino acid residues in a naturally

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occurring allergen which are conserved with more than 70% identity in all known homologous proteins within the taxonomic order from which said naturally occurring allergen originates;

5

b) defining at least one patch of conserved amino acid residues being coherently connected over at least 400 Å² of the surface of the three-dimensional structure of the allergen molecule as defined by having a solvent accessibility of at least 20 %, said at least one patch comprising at least one B cell epitope, and

10

c) substituting at least one amino acid residue in said at least one patch by another amino acid being non-conservative in the particular position while essentially preserving the overall α -carbon backbone tertiary structure of the allergen molecule.

15

In this method the best results are obtained by ranking the amino acid residues of said at least one patch with respect to solvent accessibility and substituting one or more amino acids among the more solvent accessible ones.

20

Generally, in the method according to the invention the substitution of one or more amino acid residues in said B cell epitope or said at least one patch is carried out by site-directed mutagenesis.

25

Conservation of α -carbon backbone tertiary structure is best determined by obtaining identical structures by x-ray crystallography or NMR before and after mutagenesis. In absence of structural data describing the mutant indistinguishable CD-spectra or immunochemical data, e.g. antibody reactivity, may render conservation of α -carbon backbone tertiary structure probable, if compared to the data obtained by analysis of a structurally determined

30

35

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molecule.

Further, the present invention provides a pharmaceutical composition comprising a recombinant allergen as defined
5 herein in combination with a pharmaceutically acceptable carrier and/or excipient, and optionally an adjuvant.

Such pharmaceutical composition may be in the form of a vaccine against allergic reactions elicited by a
10 naturally occurring allergen in patients suffering from allergy.

In a further aspect, the present invention relates to a method of generating an immune response in a subject,
15 which method comprises administering to the subject at least one recombinant allergen as defined herein, or a pharmaceutical composition comprising at least one recombinant allergen as defined herein.

20 The pharmaceutical composition of the invention can be prepared by a process comprising mixing at least one recombinant allergen as defined herein with pharmaceutically acceptable substances and/or excipients.

25 In a particular embodiment, the present invention concerns the vaccination or treatment of a subject, which vaccination or treatment comprises administering to the subject at least one recombinant allergen as defined herein or a pharmaceutical composition as defined herein.

30 The pharmaceutical compositions of the invention are obtainable by the process defined above.

In another embodiment, the recombinant allergens of the
35 invention are suitable for use in a method for the treatment, prevention or alleviation of allergic

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reactions, such method comprising administering to a subject a recombinant allergen as defined herein or a pharmaceutical composition as defined herein.

5 DETAILED DESCRIPTION OF THE INVENTION

Criteria for substitution

10 For molecules for which the tertiary structure has been determined (e.g. by x-ray crystallography, or NMR electron microscopy), the mutant carrying the substituted amino acid(s) should preferably fulfil the following criteria:

15 1. The overall α -carbon backbone tertiary structure of the molecule should be conserved. Conserved is defined as an average root mean square deviation of the atomic coordinates comparing the structures below 2Å. This is important for two reasons: a) It is anticipated that the
20 entire surface of the natural allergen constitutes an overlapping continuum of potential antibody-binding epitopes. The majority of the surface of the molecule is not affected by the substitution(s), and thus retain its antibody-binding properties, which is important for the
25 generation of new protective antibody specificities being directed at epitopes present also on the natural allergen. b) Stability, both concerning shelf-life and upon injection into body fluids.

30 2. The amino acid(s) to be substituted should be located at the surface, and thus be accessible for antibody-binding. Amino acids located on the surface are defined as amino acids in the three-dimensional structure having a solvent (water) accessibility of at least 20%, suitably
35 20-80%, more suitably 30-80%. Solvent accessibility is defined as the area of the molecule accessible to a

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sphere with a radius comparable to a solvent (water, $r = 1.4 \text{ \AA}$) molecule.

3. The substituted amino acid(s) should be located in
5 conserved patches larger than 400 \AA^2 . Conserved patches
are defined as coherently connected areas of surface
exposed conserved amino acid residues and backbone.
Conserved amino acid residues are defined by sequence
alignment of all known (deduced) amino acid sequences of
10 homologues proteins within the taxonomical order. Amino
acid positions having identical amino acid residues in
more than 90% of the sequences are considered conserved.
Conserved patches are expected to contain epitopes to
which the IgE of the majority of patients is directed.

15 4. Within the conserved patches amino acids for
mutagenesis should preferentially be selected among the
most solvent (water) accessible ones located preferably
near the centre of the conserved patch.

20 Preferentially, a polar amino acid residue is substituted
by another polar residue, and a non-polar amino acid
residue is substituted by another non-polar residue.

25 Preparation of vaccines is generally well-known in the
art. Vaccines are typically prepared as injectables
either as liquid solutions or suspensions. Such vaccine
may also be emulsified or formulated so as to enable
nasal administration. The immunogenic component in
30 question (the recombinant allergen as defined herein) may
suitably be mixed with excipients which are
pharmaceutically acceptable and further compatible with
the active ingredient. Examples of suitable excipients
are water, saline, dextrose, glycerol, ethanol and the
35 like as well as combinations thereof. The vaccine may
additionally contain other substances such as wetting

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(e.g. Fluosol-DA) used as a block substitute may also be employed. Other adjuvants such as Freund's complete and incomplete adjuvants as well as QuilA and RIBI may also be used.

5

Most often, multiple administrations of the vaccine will be necessary to ensure an effect. Frequently, the vaccine is administered as an initial administration followed by subsequent inoculations or other administrations. The
 10 number of vaccinations will typically be in the range of from 1 to 50, usually not exceeding 35 vaccinations. Vaccination will normally be performed from biweekly to bimonthly for a period of 3 months to 5 years. This is contemplated to give desired level of prophylactic or
 15 therapeutic effect.

The recombinant allergen may be used as a pharmaceutical preparation, which is suitable for providing a certain protection against allergic responses during the period
 20 of the year where symptoms occur (prophylaxis). Usually, the treatment will have to be repeated every year to maintain the protective effect. Preparations formulated for nasal application are particular suited for this purpose.

25

The present invention is further illustrated by the following non-limiting examples.

EXAMPLES

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EXAMPLE 1

Identification of common epitopes within *Fagales* pollen allergens

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The major birch pollen allergen *Bet v 1* shows about 90%

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amino acid sequence identity with major allergens from
pollens of taxonomically related trees, i.e *Fagales* (for
instance hazel and hornbeam) and birch pollen allergic
patients often show clinical symptoms of allergic cross-
5 reactivity towards these *Bet v 1* homologous proteins.

Bet v 1 also shows about 50-60% sequence identity with
allergic proteins present in certain fruits (for instance
apple and cherry) and vegetables (for instance celery and
10 carrot) and there are clinical evidence for allergic
cross-reactivity between *Bet v 1* and these food related
proteins.

In addition, *Bet v 1* shares significant sequence identity
15 (20-40%) with a group of plant proteins called
pathogenesis-related proteins (PR-10), however there are
no reports of allergic cross-reactivity towards these PR-
10 proteins.

20 Molecular modelling suggests that the structures of
Fagales and food allergens and PR-10 proteins are close
to be identical with the *Bet v 1* structure.

The structural basis for allergic *Bet v 1* cross-
25 reactivity was reported in (Gajhede et al 1996, ref. 17)
where three patches on the molecular surface of *Bet v 1*
could be identified to be common for the known major tree
pollen allergens. Thus, any IgE recognising these patches
on *Bet v 1* would be able to cross-react and bind to other
30 *Fagales* major pollen allergens and give rise to allergic
symptoms. The identification of these common patches was
performed after alignment of all known amino acid
sequences of the major tree pollen allergens in
combination with an analysis of the molecular surface of
35 *Bet v 1* revealed by the α -carbon backbone tertiary
structure reported in ref. 17. In addition, the patches

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Sequence alignment

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Cloning of the gene encoding Bet v 1

RNA was prepared from *Betula verrucosa* pollen (Allergon, Sweden) by phenol extraction and LiCl precipitation. Oligo(dT)-cellulose affinity chromatography was performed batch-wise in Eppendorph tubes, and double-stranded cDNA was synthesised using a commercially available kit (Amersham). DNA encoding *Bet v 1* was amplified by PCR and cloned. In brief, PCR was performed using cDNA as template, and primers designed to match the sequence of the cDNA in positions corresponding to the amino terminus of *Bet v 1* and the 3'-untranslated region, respectively. The primers were extended in the 5'-ends to accommodate restriction sites (*Nco*I and *Hind*III) for directional cloning into pKK233-2.

Subcloning into pMAL-c

The gene encoding *Bet v 1* was subsequently subcloned into the maltose binding protein fusion vector pMAL-c (New England Biolabs). The gene was amplified by PCR and subcloned in frame with *malE* to generate maltose binding protein (MBP)-*Bet v 1* protein fusion operons in which MBP and *Bet v 1* were separated by a factor X_a protease cleavage site positioned to restore the authentic aminoterminal sequence of *Bet v 1* upon cleavage, as described in ref. 15. In brief, PCR was performed using pKK233-3 with *Bet v 1* inserted as template and primers corresponding to the amino- and carboxyterminus of the protein, respectively. The promoter proximal primer was extended in the 5'-end to accommodate 4 codons encoding an in frame factor X_a protease cleavage site. Both primers were furthermore extended in the 5'-ends to accommodate restriction sites (*KpnI*) for cloning. The

Bet v 1 encoding genes were subcloned using 20 cycles of PCR to reduce the frequency of PCR artefacts.

In vitro mutagenesis

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In vitro mutagenesis was performed by PCR using recombinant pMAL-c with *Bet v 1* inserted as template. Each mutant *Bet v 1* gene was generated by 3 PCR reactions using 4 primers.

10

Two mutation-specific oligonucleotide primers were synthesised accommodating each mutation, one for each DNA strand, see Figs. 1 and 2, Using the mutated nucleotide(s) as starting point both primers were
15 extended 7 nucleotides in the 5'-end and 15 nucleotides in the 3'-end. The extending nucleotides were identical in sequence to the *Bet v 1* gene in the actual region.

Two generally applicable primers (denoted "all-sense" and
20 "all non-sense" in Figure 2) were furthermore synthesised and used for all mutants. These primers were 15 nucleotides in length and correspond in sequence to regions of the pMAL-c vector approximately 1 kilobase upstream and downstream from the *Bet v 1*. The sequence of
25 the upstream primer is derived from the sense strand and the sequence of the downstream primer is derived from the non-sense strand, see Fig. 2.

Two independent PCR reactions were performed essentially
30 according to standard procedures (Saiki et al 1988, ref. 20) with the exception that only 20 temperature cycles were performed in order to reduce the frequency of PCR artefacts. Each PCR reaction used pMAL-c with *Bet v 1* inserted as template and one mutation-specific and one
35 generally applicable primer in meaningful combinations.

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Introduction of the four amino acid substitutions (Asn28Thr, Lys32Gln, Glu45Ser, Pro108Gly) in the Triple-patch mutant were performed like described above in a step by step process. First the Glu45Ser mutation then
 5 the Pro108Gly mutation and last the Asn28Thr, Lys32Gln mutations were introduced using pMAL-c with inserted *Bet v 1* No. 2801, *Bet v 1* (Glu45Ser), *Bet v 1* (Glu45Ser, Pro108Gly) as templates, respectively.

10 The PCR products were purified by agarose gel electrophoresis and electro-elution followed by ethanol precipitation. A third PCR reaction was performed using the combined PCR products from the first two PCR reactions as template and both generally applicable
 15 primers. Again, 20 cycles of standard PCR were used. The PCR product was purified by agarose gel electrophoresis and electro-elution followed by ethanol precipitation, cut with restriction enzymes (*BsiWI/EcoRI*), and ligated directionally into pMAL-c with *Bet v 1* inserted
 20 restricted with the same enzymes.

Figure 3 shows an overview of all 9 *Bet v 1* mutations, which are as follows

25 Thr10Pro, Asp25Gly, Asn28Thr + Lys32Gln, Glu45Ser, Asn47Ser, Lys55Asn, Glu60Ser (non-patch), Thr77Ala and Pro108Gly. An additional four mutant with four mutations was also prepared (Asn28Thr, Lys32Gln, Glu45Ser, Pro108Gly). Of these, five were selected for further
 30 testing: Asn28Thr + Lys32Gln, Glu45Ser, Glu60Ser, Pro108Gly and the Triple-patch mutant Asn28Thr, Lys32Gln, Glu45Ser, Pro108Gly.

Nucleotide sequencing

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Determination of the nucleotide sequence of the *Bet v 1*

encoding gene was performed before and after subcloning, and following *in vitro* mutagenesis, respectively.

Plasmid DNA's from 10 ml of bacterial culture grown to saturation overnight in LB medium supplemented with 0.1 g/l ampicillin were purified on Qiagen-tip 20 columns and sequenced using the Sequenase version 2.0 DNA sequencing kit (USB) following the recommendations of the suppliers.

10 Expression and purification of recombinant Bet v 1 and mutants

Recombinant Bet v 1 (Bet v 1 No. 2801 and mutants) were over-expressed in *Escherichia coli* DH 5a fused to maltose-binding protein and purified as described in ref. 15. Briefly, recombinant *E.coli* cells were grown at 37°C to an optical density of 1.0 at 436 nm, whereupon expression of the Bet v 1 fusion protein was induced by addition of IPTG. Cells were harvested by centrifugation 3 hours post-induction, re-suspended in lysis buffer and broken by sonication. After sonication and additional centrifugation, recombinant fusion protein was isolated by amylose affinity chromatography and subsequently cleaved by incubation with Factor Xa (ref. 15). After F Xa cleavage, recombinant Bet v 1 was isolated by gelfiltration and if found necessary, subjected to another round of amylose affinity chromatography in order to remove trace amounts of maltose-binding protein.

Purified recombinant Bet v 1 was concentrated by ultrafiltration to about 5 mg/ml and stored at 4 °C. The final yields of the purified recombinant Bet v 1 preparations were between 2-5 mg per litre *E. coli* cell culture.

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The purified recombinant Bet v 1 preparations appeared as

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single bands after silver-stained SDS-polyacrylamide electrophoresis with an apparent molecular weight of 17.5 kDa. N-terminal sequencing showed the expected sequences as derived from the cDNA nucleotide sequences and
 5 quantitative amino acid analysis showed the expected amino acid compositions.

We have previously shown (ref. 15) that recombinant Bet v 1 No. 2801 is immunochemically indistinguishable from
 10 naturally occurring Bet v 1.

Immuno-electrophoresis using rabbit polyclonal antibodies

The seven mutant Bet v 1 were produced as recombinant Bet
 15 v 1 proteins and purified as described above and tested for their reactivity towards polyclonal rabbit antibodies raised against Bet v 1 isolated from birch pollen. When analysed by immuno-electrophoresis (rocket-line immuno-electrophoresis) under native conditions, the
 20 rabbit antibodies were able to precipitate all mutants, indicating that the mutants had conserved α -carbon backbone tertiary structure.

These results suggested that non-naturally occurring
 25 substitutions introduced on the molecular surface of Bet v 1 can reduce a polyclonal antibody response raised against naturally occurring Bet v 1 without distortion of the overall α -carbon backbone tertiary allergen structure. In order to analyse the effect on human
 30 polyclonal IgE-response, the mutants Glu45Ser, Pro108Gly, Asn28Thr+Lys32Gln and Glu60Ser were selected for further analysis.

Bet v 1 Glu45Ser mutant

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Glutamic acid in position 45 show a high degree of

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solvent-exposure (40%) and is located in a molecular surface patch common for *Fagales* allergens (patch I). A serine residue was found to occupy position 45 in some of the *Bet v 1* homologous PR-10 proteins arguing for that glutamic acid can be replaced by serine without distortion of the α -carbon backbone tertiary structure. In addition, as none of the known *Fagales* allergen sequences have serine in position 45, the substitution of glutamic acid with serine gives rise to a non-naturally occurring *Bet v 1* molecule.

T cell proliferation assay using recombinant Glu45Ser *Bet v 1* mutant

The analysis was carried out as described in Spangfort et al 1996a. It was found that recombinant *Bet v 1* Glu45Ser mutant was able to induce proliferation in T cell lines from three different birch pollen allergic patients with stimulation indices similar to recombinant and naturally occurring.

Crystallisation and structural determination of recombinant Glu45Ser *Bet v 1*

Crystals of recombinant Glu45Ser *Bet v 1* were grown by vapour diffusion at 25°C, essentially as described in (Spangfort et al 1996b, ref. 21). Glu45Ser *Bet v 1*, at a concentration of 5 mg/ml, was mixed with an equal volume of 2.0 M ammonium sulphate, 0.1 M sodium citrate, 1% (v/v) dioxane, pH 6.0 and equilibrated against 100x volume of 2.0 M ammonium sulfate, 0.1 M sodium citrate, 1% (v/v) dioxane, pH 6.0. After 24 hours of equilibration, crystal growth was induced by applying the seeding technique described in ref. 21, using crystals of recombinant wild-type *Bet v 1* as a source of seeds.

After about 2 months, crystals were harvested and analysed using X-rays generated from a Rigaku rotating anode as described in ref. 21 and the structure was solved using molecular replacement.

5

Structure of Bet v 1 Glu45Ser mutant

The structural effect of the mutation was addressed by growing three-dimensional Bet v 1 Glu45Ser protein crystals diffracting to 3.0 Å resolution when analysed by X-rays generated from a rotating anode. The substitution of glutamic acid to serine in position 45 was verified by the Bet v 1 Glu45Ser structure electron density map which also showed that the overall α -carbon backbone tertiary structure is preserved.

15

IgE-binding properties of Bet v 1 Glu45Ser mutant

The IgE-binding properties of Bet v 1 Glu45Ser mutant was compared with recombinant Bet v 1 in a fluid-phase IgE-inhibition assay using a pool of serum IgE derived from birch allergic patients.

20

Recombinant Bet v 1 no. 2801 was biotinylated at a molar ratio of 1:5 (Bet v 1 no. 2801:biotin). The inhibition assay was performed as follows: a serum sample (25 μ l) was incubated with solid phase anti IgE, washed, re-suspended and further incubated with a mixture of biotinylated Bet v 1 no. 2801 (3.4 nM) and a given mutant (0-28.6 nM). The amount of biotinylated Bet v 1 no. 2801 bound to the solid phase was estimated from the measured RLU after incubation with acridinium ester labelled streptavidin. The degree of inhibition was calculated as the ratio between the RLU's obtained using buffer and mutant as inhibitor.

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Figure 4 shows the inhibition of the binding of biotinylated recombinant *Bet v 1* to serum IgE from a pool of allergic patients by non-biotinylated *Bet v 1* and by *Bet v 1* Glu45Ser mutant.

5

There is a clear difference in the amount of respective recombinant proteins necessary to reach 50% inhibition of the binding to serum IgE present in the serum pool. Recombinant *Bet v 1* reaches 50% inhibition at about 6.5
 10 ng whereas the corresponding concentration for *Bet v 1* Glu45Ser mutant is about 12 ng. This show that the point mutation introduced in *Bet v 1* Glu45Ser mutant lowers the affinity for specific serum IgE by a factor of about 2. The maximum level of inhibition reached by the *Bet v 1*
 15 Glu45Ser mutant is clearly lower compared to recombinant *Bet v 1*. This may indicate that after the Glu45Ser substitution, some of the specific IgE present in the serum pool are unable to recognise the *Bet v 1* Glu45Ser mutant.

20

Bet v 1 mutant Asn28Thr+Lys32Gln

Aspartate and lysine in positions 28 and 32, respectively show a high degree of solvent-exposure (35% and 50%,
 25 respectively) and are located in a molecular surface patch common for *Fagales* allergens (patch II). In the structure, aspartate 28 and lysine 32 are located close to each other on the molecular surface and most likely interact via hydrogen bonds. A threonine and a glutamate
 30 residue were found to occupy positions 28 and 32, respectively in some of the *Bet v 1* homologous PR-10 proteins arguing for that aspartate and lysine can be replaced with threonine and glutamate, respectively without distortion of the α -carbon backbone tertiary
 35 structure. In addition, as none of the naturally occurring isoallergen sequences have threonine and

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glutamate in positions 28 and 32, respectively, the substitutions gives rise to a non-naturally occurring *Bet v 1* molecule.

5 IgE-binding properties of *Bet v 1* mutant
Asn28Thr+Lys32Gln

The IgE-binding properties of mutant Asn28Thr+Lys32Gln was compared with recombinant *Bet v 1* in a fluid-phase
 10 IgE-inhibition assay using the pool of serum IgE derived from birch allergic patients described above.

Figure 5 shows the inhibition of the binding of biotinylated recombinant *Bet v 1* to serum IgE from a pool
 15 of allergic patients by non-biotinylated *Bet v 1* and by *Bet v 1* mutant Asn28Thr+Lys32Gln.

There is a clear difference in the amount of respective recombinant proteins necessary to reach 50% inhibition of
 20 the binding to serum IgE present in the serum pool. Recombinant *Bet v 1* reaches 50% inhibition at about 6.5 ng whereas the corresponding concentration for *Bet v 1* mutant Asn28Thr+Lys32Gln is about 12 ng. This show that the point mutations introduced in *Bet v 1* mutant
 25 Asn28Thr+Lys32Gln lowers the affinity for specific serum IgE by a factor of about 2.

The maximum level of inhibition reached by the *Bet v 1* mutant Asn28Thr+Lys32Gln mutant is clearly lower compared
 30 to recombinant *Bet v 1*. This may indicate that after the Asn28Thr+Lys32Gln substitutions, some of the specific IgE present in the serum pool are unable to recognise the *Bet v 1* mutant Asn28Thr+Lys32Gln.

35 *Bet v 1* mutant Pro108Gly

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Proline in position 108 show a high degree of solvent-exposure (60%) and is located in a molecular surface patch common for *Fagales* allergens (patch III). A glycine residue was found to occupy position 108 in some of the
 5 *Bet v 1* homologous PR-10 proteins arguing for that proline can be replaced with glycine without distortion of the α -carbon backbone tertiary structure. In addition, as none of the naturally occurring isoallergen sequences have glycine in position 108, the substitution of proline
 10 with glycine gives rise to a non-naturally occurring *Bet v 1* molecule.

IgE-binding properties of *Bet v 1* Pro108Gly mutant

- 15 The IgE-binding properties of *Bet v 1* Pro108Gly mutant was compared with recombinant *Bet v 1* in a fluid-phase IgE-inhibition assay using the pool of serum IgE derived from birch allergic patients described above.
- 20 Figure 6 shows the inhibition of the binding of biotinylated recombinant *Bet v 1* to serum IgE from a pool of allergic patients by non-biotinylated *Bet v 1* and by *Bet v 1* Pro108Gly mutant.
- 25 There is a clear difference in the amount of respective recombinant proteins necessary to reach 50% inhibition of the binding to serum IgE present in the serum pool. Recombinant *Bet v 1* reaches 50% inhibition at about 6.5 ng whereas the corresponding concentration for *Bet v 1*
 30 Pro108Gly is 15 ng. This show that the single point mutation introduced in *Bet v 1* Pro108Gly lowers the affinity for specific serum IgE by a factor of about 2.

The maximum level of inhibition reached by the *Bet v 1*
 35 Pro108Gly mutant is somewhat lower compared to recombinant *Bet v 1*. This may indicate that after the

Pro108Gly substitution, some of the specific IgE present in the serum pool are unable to recognise the Bet v 1 Pro108Gly mutant.

5 Bet v 1 mutant Glu60Ser (non-patch mutant)

Glutamic acid in position 60 show a high degree of solvent-exposure (60%) however, it is not located in a molecular surface patch common for *Fagales* allergens. A
 10 serine residue was found to occupy position 60 in some of the Bet v 1 homologous PR-10 proteins arguing for that glutamic acid can be replaced with serine without distortion of the α -carbon backbone tertiary structure. In addition, as none of the naturally occurring
 15 isoallergen sequences have serine in position 60, the substitution of glutamic acid with serine gives rise to a non-naturally occurring Bet v 1 molecule.

IgE-binding properties of Bet v 1 Glu60Ser mutant

20 The IgE-binding properties of Bet v 1 Glu60Ser mutant was compared with recombinant Bet v 1 in a fluid-phase IgE-inhibition assay using the pool of serum IgE derived from birch allergic patients described above.

25 Figure 7 shows the inhibition of the binding of biotinylated recombinant Bet v 1 to serum IgE from a pool of allergic patients by non-biotinylated Bet v 1 and by Bet v 1 Glu60Ser mutant. In contrast to the Glu45Ser,
 30 Pro108Gly and Asn28Thr+Lys32Gln mutants, the substitution glutamic acid 60 to serine, does not shown any significant effect on the IgE-binding properties of. This indicates that substitutions outside the defined *Fagales* common patches only have a marginal effect on the binding
 35 of specific serum IgE supporting the concept that conserved allergen molecular surface areas harbours

dominant IgE-binding epitopes.

Bet v 1 Triple-patch mutant

5 In the Triple-patch mutant, the point mutations (Glu45Ser, Asn28Thr+Lys32Gln and Pro108Gly) introduced in the three different common *Fagales* patches, described above, were simultaneously introduced in creating an artificial mutant carrying four amino acid substitutions.

10

Structural analysis of Bet v 1 Triple-patch mutant

The structural integrity of the purified Triple-patch mutant was analysed by circular dichroism (CD) spectroscopy. Figure 8 shows the CD spectra of recombinant and Triple-patch mutant, recorded at close to equal concentrations. The overlap in peak amplitudes and positions in the CD spectra from the two recombinant proteins shows that the two preparations contain equal amounts of secondary structures strongly suggesting that the α -carbon backbone tertiary structure is not affected by the introduced amino acid substitutions.

20

IgE-binding properties of Bet v 1 Triple-patch mutant

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The IgE-binding properties of Bet v 1 Triple-patch mutant was compared with recombinant Bet v 1 in a fluid-phase IgE-inhibition assay using the pool of serum IgE derived from birch allergic patients described above.

30

Figure 9 shows the inhibition of the binding of biotinylated recombinant Bet v 1 to serum IgE from a pool of allergic patients by non-biotinylated Bet v 1 and by Bet v 1 Triple-patch mutant. In contrast to the single mutants described above, the inhibition curve of the Triple-patch mutant is no longer parallel relative to

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recombinant. This shows that the substitutions introduced in the Triple-patch mutant has changed the IgE-binding properties and epitope profile compared to recombinant. The lack of parallellity makes it difficult to quantify the decrease of the Triple-patch mutant affinity for specific serum IgE.

Recombinant Bet v 1 reaches 50% inhibition at about 6 ng whereas the corresponding concentration for Bet v 1 Triple-patch mutant is 30 ng, i.e a decrease in affinity by a factor 5. However, in order to reach 80% inhibition the corresponding values are 20 ng and 400 ng, respectively, i.e a decrease by a factor 20.

T cell proliferation assay using recombinant Bet v 1 Triple-patch mutant

The analysis was carried out as described in ref. 15. It was found that recombinant Bet v 1 Triple-patch mutant was able to induce proliferation in T cell lines from three different birch pollen allergic patients with stimulation indices similar to recombinant and naturally occurring. This suggests that the Triple-patch mutant can initiate the cellular immune response necessary for antibody production.

EXAMPLE 2

Identification of common epitopes within *Vespula vulgaris* venom major allergen antigen 5

Antigen 5 is one of the three vespid venom proteins, which are known allergens in man. The vespids include hornets, yellow-jacket and wasps. The other two known allergens of vespid venoms are phospholipase A₁ and hyaluronidase. Antigen 5 from *Vespula vulgaris* (Ves v 5)

has been cloned and expressed as recombinant protein in the yeast system (Monsalve et al. 1999, ref. 22). The three-dimensional crystal structure of recombinant Ves v 5 has recently been determined at 1.8 Å resolution (in preparation). The main features of the structure consist of four β -strands and four α -helices arranged in three stacked layers giving rise to a " α - β - α sandwich". The sequence identity between Antigen 5 homologous allergens from different *Vespula* species is about 90% suggesting presence of conserved molecular surface areas and B cell epitopes.

The presence and identification of common patches was performed after alignment of all known amino acid sequences, as previously described for tree pollen allergens, of the *Vespula* antigen 5 allergens in combination with an analysis of the molecular surface of Antigen 5 revealed by the three-dimensional structure of Ves v 5. Figure 10 shows solvent accessibility of individually aligned antigen 5 residues and alignment of *Vespula* antigen 5 sequences (left panel). On the right panel of figure 10 is shown the molecular surface of antigen 5 with conserved areas among *Vespula* antigen 5:s coloured.

Selection of amino acid residues for site-directed mutagenesis

Amino acid residues for site-directed mutagenesis were selected among residues present the patches common for *Vespula* since modifications of these is expected to affect the binding of serum IgE from the majority of patients showing clinical *Vespula* allergic cross-reactivity.

The relative orientation and percentage of solvent-

exposure of each amino acid residue within respective patch was calculated based on their atomic coordinates. Residues having a low degree of solvent exposure were not regarded suitable for mutagenesis due to the possible
 5 disruption of the structure or lack of antibody interaction. The remaining residues were ranked according to their degree of solvent-exposure.

Cloning of the gene encoding Ves v 5

10

Total RNA was isolated from venom acid glands of *Vespula vulgaris* vespids as described in (Fang et al. 1988, ref. 23).

15 First-strand cDNA synthesis, PCR amplification and cloning of the Ves v 5 gene was performed as described in (Lu et al. 1993, ref. 24)

Subcloning into pPICZ α A

20

The gene encoding Ves v 5 was subsequently sub-cloned into the pPICZ α A vector (Invitrogen) for secreted expression of Ves v 5 in *Pichia pastoris*. The gene was amplified by PCR and sub-cloned in frame with the coding
 25 sequence for the α -factor secretion signal of *Saccharomyces cerevisiae*. In this construct the α -factor is cleaved off, *in vivo*, by the *Pichia pastoris* Kex2 protease system during secretion of the protein.

30 In brief PCR was performed using Ves v 5 as template and primers corresponding to the amino- and carboxyterminus of the protein, respectively. The primers were extended in the 5'-end to accommodate restriction sites for cloning, EcoRI and XbaI, respectively. Nucleotides
 35 encoding the Kex2 cleavage site was in this construct positioned 18 nucleotides upstream to the amino terminus

of the protein, resulting in the expression of Ves v 5 with six additional amino acids, Glu-Ala-Glu-Ala-Glu-Phe, at the amino terminus.

5 Insertion of pPICZ α A-Ves v 5 into *P. pastoris*

The pPICZ α A vectors with the Ves v 5 gene inserted was linearised by Sac I restriction and inserted into the AOX1 locus on the *Pichia pastoris* genome. Insertion was performed by homologous recombination on *Pichia pastoris* 10 KM71 cells following the recommendations of Invitrogen.

In vitro mutagenesis

15 *In vitro* mutagenesis was performed by PCR using recombinant pPICZ α A with Ves v 5 inserted as template. Each mutant Ves v 5 gene was generated by 3 PCR reactions using 4 primers.

20 Two mutation-specific oligonucleotide primers were synthesised accommodating each mutation, one for each DNA strand, see Figures 11 and 12. Using the mutated nucleotide(s) as starting point both primers were extended 6-7 nucleotides in the 5'-end and 12-13 25 nucleotides in the 3'-end. The extending nucleotides were identical in sequence to the Ves v 5 gene in the actual region.

Two generally applicable primers (denoted "all sense" and 30 "all non-sense" in Figure 12) were furthermore synthesised and used for all mutants. To insure expression of Ves v 5 mutants with authentic amino terminus, one primer corresponding to the amino terminus of the protein was extended in the 5'-end with a Xho I 35 site. Upon insertion of the Ves v 5 mutant genes into the pPICZ α A vector, the Kex2 protease cleavage site was

regenerated directly upstream to the amino terminus of Ves v 5. The second primer was corresponding in sequence to a region of the pPICZ α A vector positioned approximately 300 bp downstream from the Ves v 5 gene.

5 The sequence of the primer corresponding to the amino terminus of Ves v 5 is derived from the sense strand and the sequence of the downstream primer is derived from the non-sense strand, see Figure 11.

10 Two independent PCR reactions were performed essentially according to standard procedures (Saiki et al 1988) with the exception that only 20 temperature cycles were performed in order to reduce the frequency of PCR artefacts. Each PCR reaction used pPICZ α A with Ves v 5
15 inserted as template and one mutation-specific and one generally applicable primer in meaningful combinations.

The PCR products were purified by using "Concert, Rapid PCR Purification System" (Life Technologies). A third PCR
20 reaction was performed using the combined PCR products from the first two PCR reactions as template and both generally applicable primers. Again, 20 cycles of standard PCR were used. The PCR product was purified with the "Concert, Rapid PCR Purification System" (Life
25 Technologies), cut with restriction enzymes (*XhoI/XbaI*), and ligated directionally into pPICZ α A vector restricted with the same enzymes. Figure 13 shows an overview of all Ves v 5 mutations.

30 Insertion of pPICZ α A-Ves v 5 mutants into *P. pastoris*

The pPICZ α A vectors with the Ves v 5 mutant genes inserted were linearised by Sac I restriction and inserted into the AOX1 locus on the *Pichia pastoris*
35 genome. Insertions were performed by homologous recombination on *Pichia pastoris* KM71 cells following the

recommendations of Invitrogen.

Nucleotide sequencing

- 5 Determination of the nucleotide sequence of the Ves v 5 encoding gene was performed before and after subcloning, and following *in vitro* mutagenesis, respectively.

10 Plasmid DNA's from 10 ml of bacterial culture grown to saturation overnight in LB medium supplemented with 0.1 g/l ampicillin were purified on Qiagen-tip 20 columns and sequenced using the Sequenase version 2.0 DNA sequencing kit (USB) following the recommendations of the suppliers.

15 Expression and purification of recombinant Ves v 5

Recombinant yeast cells of *Pichia pastoris* strain KM71 were grown in 500 ml bottles containing 100 ml of pH 6.0 phosphate buffer containing yeast nitrogen base, biotin, glycerol and histidine at 30°C with orbital shaking at 225 rpm until A_{600} nm of 4-6. Cells were collected by centrifugation and re-suspended in 10 ml of similar buffered medium containing methanol in place of glycerol. Incubation was continued at 30°C for 7 days with daily addition of 0.05 ml methanol.

Cells were harvested by centrifugation and the collected culture fluid was concentrated by ultrafiltration. After dialysis against 50 mM ammonium acetate buffer, pH 4.6, the sample was applied to a FPLC (Pharmacia) SE-53 cation exchange column equilibrated in the same buffer. The column was eluted with a 0-1.0 M NaCl, 50 mM ammonium acetate linear gradient. The recombinant Ves v 5 peak eluting at about 0.4 M NaCl was collected and dialysed against 0.02 N acetic acid. After concentration to about 10 mg/ml, the purified Ves v 5 was stored at 4°C.

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Crystallisation of recombinant Ves v 5

Crystals of Ves v 5 was grown by the vapour diffusion technique at 25°C. For crystallisation, 5 µl of 5 mg/ml Ves v 5 was mixed with 5 µl of 18% PEG 6000, 0.1 M sodium citrate, pH 6.0 and equilibrated against 1 ml of 18% PEG 6000, 0.1 M sodium citrate, pH 6.0.

X-ray diffraction data was collected at 100K from native Ves v 5 crystals and after incorporation of heavy-atom derivatives and used to solve the three-dimensional structure of Ves v 5, see Figure 10 (manuscript in preparation).

Immunoelectrophoresis using rabbit polyclonal antibodies

The two Ves v 5 mutants were produced as recombinant Ves v 5 proteins and tested for their reactivity towards polyclonal rabbit antibodies raised against recombinant Ves v 5. When analysed by rocket immunoelectrophoresis under native conditions, the rabbit antibodies were able to precipitate recombinant Ves v 5 as well as both mutants, indicating that the mutants have conserved α -carbon backbone tertiary structure.

Inhibition of specific serum IgE

The IgE-binding properties of Ves v 5 mutants were compared to recombinant Ves v 5 in a fluid-phase IgE-inhibition assay using a pool of serum IgE derived from vespid venom allergic patients.

The inhibition assay was performed as described above using biotinylated recombinant Ves v 5 instead of Bet v 1.

Ves v 5 Lys72Ala mutant

Lysine in position 72 show a high degree of solvent-exposure (70%) and is located in a molecular surface patch common for *Vespula* antigen 5. The relative orientation and high degree of solvent exposure argued for that lysine 72 can be replaced by an alanine residue without distortion of the α -carbon backbone tertiary structure. In addition, as none of the naturally occurring isoallergen sequences have alanine in position 72, the substitution of lysine with alanine gives rise to a non-naturally occurring Ves v 5 molecule.

IgE-binding properties of Ves v 5 Lys72Ala mutant

The IgE-binding properties of Ves v 5 Lys72Ala mutant was compared with recombinant Ves v 5 in a fluid-phase IgE-inhibition assay using the pool of serum IgE derived from birch allergic patients described above.

Figure 14 shows the inhibition of the binding of biotinylated recombinant Ves v 5 to serum IgE from a pool of allergic patients by non-biotinylated Ves v 5 and by Ves v 5 Lys72Ala mutant.

There is a clear difference in the amount of respective recombinant proteins necessary to reach 50% inhibition of the binding to serum IgE present in the serum pool. Recombinant Ves v 5 reaches 50% inhibition at about 6 ng whereas the corresponding concentration for Ves v 5 Lys72Ala mutant is 40 ng. This show that the single point mutation introduced in Ves v 5 Lys72Ala mutant lowers the affinity for specific serum IgE by a factor of about 6. The maximum level of inhibition reached by the Ves v 5 Lys72Ala mutant significantly lower compared to

recombinant Ves v 5. This may indicate that after the Lys72Ala substitution, some of the specific IgE present in the serum pool are unable to recognise the Ves v 5 Lys72Ala mutant.

5

Ves v 5 Tyr96Ala mutant

Tyrosine in position 96 show a high degree of solvent-exposure (65%) and is located in a molecular surface patch common for *Vespula* antigen 5. The relative orientation an high degree of solvent exposure argued for that tyrosine 96 can be replaced by an alanine residue without distortion of the three-dimensional structure. In addition, as none of the naturally occurring isoallergen sequences have alanine in position 96, the substitution of tyrosine with alanine gives rise to a non-naturally occurring Ves v 5 molecule.

15

IgE-binding properties of Ves v 5 Tyr96Ala mutant

20

The IgE-binding properties of Ves v 5 Tyr96Ala mutant was compared with recombinant Ves v 5 in a fluid-phase IgE-inhibition assay using the pool of serum IgE derived from birch allergic patients described above.

25

Figure 14 shows the inhibition of the binding of biotinylated recombinant Ves v 5 to serum IgE from a pool of allergic patients by non-biotinylated Ves v 5 and by Ves v 5 Tyr96Ala mutant.

30

There is a clear difference in the amount of respective recombinant proteins necessary to reach 50% inhibition of the binding to serum IgE present in the serum pool. Recombinant Ves v 5 reaches 50% inhibition at about 6 ng whereas the corresponding concentration for Ves v 5 Tyr96Ala mutant is 40 ng.

35

This show that the single point mutation introduced in Ves v 5 Tyr96Ala mutant lowers the affinity for specific serum IgE by a factor of about 6.

5

The maximum level of inhibition reached by the Ves v 5 Tyr96Ala mutant significantly lower compared to recombinant Ves v 5. This may indicate that after the Tyr96Ala substitution, some of the specific IgE present
10 in the serum pool are unable to recognise the Ves v 5 Tyr96Ala mutant.

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CLAIMS

1. Recombinant allergen, characterised in that it is a non-naturally occurring mutant derived from a naturally occurring allergen, wherein at least one surface-exposed, conserved amino acid residue of a B cell epitope is substituted by another residue which does not occur in the same position in the amino acid sequence of any known homologous protein within the taxonomic order from which said naturally occurring allergen originates, said mutant allergen having essentially the same α -carbon backbone tertiary structure as said naturally occurring allergen, and the specific IgE binding to the mutated allergen being reduced as compared to the binding to said naturally occurring allergen.

2. Recombinant allergen according to claim 1, characterised in that it is obtainable by

a) identifying amino acid residues in a naturally occurring allergen which are conserved with more than 70% identity in all known homologous proteins within the taxonomic order from which said naturally occurring allergen originates;

b) defining at least one patch of conserved amino acid residues being coherently connected over at least 400 \AA^2 of the surface of the three-dimensional structure of the allergen molecule as defined by having a solvent accessibility of at least 20 %, said at least one patch comprising at least one B cell epitope; and

c) substituting at least one amino acid residue in said at least one patch by another amino acid being non-conservative in the particular position while essentially preserving the overall α -carbon backbone tertiary

structure of the allergen molecule.

3. Recombinant allergen according to claim 1 or 2,
characterised in that the specific IgE binding to the
5 mutated allergen is reduced by at least 5%, preferably at
least 10%.

4. Recombinant allergen according to any of claims 1-3,
characterised in that when comparing the α -carbon
10 backbone tertiary structures of the mutant and the
naturally occurring allergen molecules, the average root
mean square deviation of the atomic coordinates is below
2Å.

15 5. Recombinant allergen according to claim 2,
characterised in that said at least one patch comprises
atoms of 15-25 amino acid residues.

6. Recombinant allergen according to any one of claims
20 2-5, characterised in that the amino acid residues of
said at least one patch are ranked with respect to
solvent accessibility, and one or more amino acids among
the more solvent accessible ones are substituted.

25 7. Recombinant allergen according to claim 6,
characterised in that one or more amino acid residues of
said at least one patch having a solvent accessibility of
20-80 % are substituted.

30 8. Recombinant allergen according to any one of claims
2-7, characterised in that 1-5 amino acid residues per
400 Å² in said at least one patch are substituted.

9. Recombinant allergen according to any one of claims
35 2-5, characterised in that the substitution of one or
more amino acid residues in said B cell epitope or said

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at least one patch is carried out by site-directed mutagenesis.

10. Recombinant allergen according to any one of claims
5 1-9, characterised in that it is derived from an inhalation allergen.

11. Recombinant allergen according to claim 10,
characterised in that it is derived from a pollen
10 allergen.

12. Recombinant allergen according to claim 10,
characterised in that it is derived from a pollen
allergen originating from the taxonomic order of *Fagales*,
15 *Oleales* or *Pinales*.

13. Recombinant allergen according to claim 12,
characterised in that it is derived from *Bet v 1*.

20 14. Recombinant allergen according to claim 13,
characterised in that at least one amino acid residue of
said B cell epitope or said at least one patch is
substituted.

25 15. Recombinant allergen according to claim 14,
characterised in that the substitution(s) is (are)
Thr10Pro, Asp25Gly, (Asn28Thr + Lys32Gln), Glu45Ser,
Asn47Ser, Lys55Asn, Thr77Ala, Pro108Gly or (Asn28Thr,
Lys32Gln, Glu45Ser, Pro108Gly.

30

16. Recombinant allergen according to claim 11,
characterised in that it is derived from a pollen
allergen originating from the taxonomic order of *Poales*.

35 17. Recombinant allergen according to claim 11,
characterised in that it is derived from a pollen

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allergen originating from the taxonomic order of *Asterales* or *Urticales*.

18. Recombinant allergen according to claim 10,
5 characterised in that it is derived from a house dust mite allergen.

19. Recombinant allergen according to claim 18,
characterised in that it is derived from a mite allergen
10 originating from *Dermatophagoides*.

20. Recombinant allergen according to claim 10,
characterised in that it is derived from a cockroach
allergen.

15 21. Recombinant allergen according to claim 10,
characterised in that it is derived from an animal
allergen.

20 22. Recombinant allergen according to claim 21,
characterised in that it is derived from an animal
allergen originating from cat, dog or horse.

23. Recombinant allergen according to any one of claims
25 1-9, characterised in that it is derived from a venom
allergen.

24. Recombinant allergen according to claim 23,
characterised in that it is derived from a venom allergen
30 originating from the taxonomic order of *Hymenoptera*.

25. Recombinant allergen according to claim 24,
characterised in that it is derived from a venom allergen
from the taxonomic order of *Vespidae*, *Apidae* and
35 *Formicoidae*.

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26. Recombinant allergen according to any one of claims 23-25, characterised in that it is derived from Ves v 5.

27. Recombinant allergen according to any one of claims 23-26, characterised in that at least one amino acid is substituted.

28. Recombinant allergen according to any one of claims 25-27, characterised in that the substitution is Lys72Ala or Tyr96Ala.

29. A method of preparing a recombinant allergen according to any one of claims 1-29, characterised by

a) identifying amino acid residues in a naturally occurring allergen which are conserved with more than 70% identity in all known homologous proteins within the taxonomic order from which said naturally occurring allergen originates;

b) defining at least one patch of conserved amino acid residues being coherently connected over at least 400 Å² of the surface of three-dimensional structure of the allergen molecule as defined by having a solvent accessibility of at least 20%, said at least one patch comprising at least one B cell epitope; and

c) substituting at least one amino acid residue in said at least one patch by another amino acid being non-conservative in the particular position while essentially preserving the overall α-carbon backbone tertiary structure of the allergen molecule.

30. A method according to claim 29, characterised by ranking the amino acid residues of said at least one patch with respect to solvent accessibility and

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substituting one or more amino acids among the more solvent accessible ones.

31. A method according to claim 29 or 30, characterised
5 in that the substitution of one or more amino acid residues in said B cell epitope or said at least one patch is carried out by site-directed mutagenesis.

32. Recombinant allergen according to any of claims 1-28
10 for use as a pharmaceutical.

33. Pharmaceutical composition, characterised in that it comprises a recombinant allergen according to any one of claims 1-28, optionally in combination with a
15 pharmaceutically acceptable carrier and/or excipient, and optionally an adjuvant.

34. A pharmaceutical composition according to claim 33, characterised in that it is in the form of a vaccine
20 against allergic reactions elicited by a naturally occurring allergen in patients suffering from allergy.

35. Method of generating an immune response in a subject comprising administering to the subject at least one
25 recombinant allergen according to any one of claims 1-28 or a pharmaceutical composition according to any one of claims 33-34.

36. Process for preparing a pharmaceutical composition
30 according to any one of claims 33-34 comprising mixing at least one recombinant allergen according to any one of claims 1-28 with pharmaceutically acceptable substances and/or excipients.

37. Vaccination or treatment of a subject comprising
35 administering to the subject at least one recombinant

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allergen according to any one of claims 1-28 or a pharmaceutical composition according to any one of claims 33-34.

- 5 38. Pharmaceutical composition obtainable by the process according to claim 36.

39. Method for the treatment, prevention or alleviation of allergic reactions comprising administering to a
10 subject a recombinant allergen according to any one of claims 1-28 or a pharmaceutical composition according to any one of claims 33-34 or 38.

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ABSTRACT

NOVEL RECOMBINANT ALLERGENS

- 5 Novel recombinant allergens are disclosed. The allergens are non-naturally occurring mutants derived from naturally-occurring allergens. The overall α -carbon backbone tertiary structure is essentially preserved. Also disclosed are method for preparing such recombinant
10 allergens as well as uses thereof.

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Fig. 1

Mutant-specific oligonucleotide primers used for mutant number 1. Mutated nucleotide underlined

	10	20	30	40	50
	—	—	—	—	—
Bet v 1 sense	5'-	AATTATGAGACTGAGACC	<u>ACCT</u> TGT	TATCC	CAGCAGCTCG -3'
Bet v 1 non-sense	3'-	TTAATACTCTGACTCTGGT	<u>GG</u>	GAGACAATAGGGTCGTCGAGC	-5'
sense primer	5'-		TGAGACCC	CTCTGTTATCC	CAG -3'
non-sense primer	3'-	ATACTCTGACTCTGGG	GGG	GAGACA	-5'

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Fig. 2

Oligonucleotide primers for site directed mutagenesis of
Bet v 1 (No. 2801).

all	sense	1: 163Bv, 15-mer	5'-GTTGCCAACGATCAG
1	sense	2: 184Bv, 23-mer	5'-TGAGACCCCTCTGTTATCCCAG
1	non-sense	3: 185Bv, 23-mer	5'-ACAGAGGGGGTCTCAGTCTCATA
2	sense	4: 186Bv, 31-mer	5'-GATACCCCTCTTCCACAGGTTGCACCCCAAG
2	non-sense	5: 187Bv, 31-mer	5'-ACCTGTGGAAAGAGGGTATCGCCATCAAGGA
3	sense	6: 188Bv, 23-mer	5'-AACATTTCAGGAAATGGAGGGCC
3	non-sense	7: 189Bv, 23-mer	5'-TTTCCTGAAATGTTTCAACACT
4	sense	8: 190Bv, 23-mer	5'-TTAAGAACATCAGCTTCCCCGAA
4	non-sense	9: 191Bv, 23-mer	5'-AGCTGATGTTCTTAATGGTTCCA
5	sense	10: 192Bv, 23-mer	5'-GGACCATGCAAACTTCAAATACA
5	non-sense	11: 193Bv, 23-mer	5'-AGTTTGCAATGGTCCACCTCATCA
6	sense	12: 194Bv, 23-mer	5'-TTTCCCTCAGGCCCTCCCTTTCAA
6	non-sense	13: 195Bv, 23-mer	5'-AGGCCTGAGGGAAAGCTGATCTT
7	sense	14: 196Bv, 24-mer	5'-TGAAGGATCTGGAGGGCCTGGAAC
7	non-sense	15: 197Bv, 24-mer	5'-CGCTCCAGATCCTTCAATGTTTTC
8	sense	16: 198Bv, 24-mer	5'-GGCAACTGGTGAATGGAGGATCCAT
8	non-sense	17: 199Bv, 24-mer	5'-CCATCACCAGTTGCCACTATCTTT
all	non-sense	18: 200Bv, 15-mer	5'-CATGCCATCCGTAAG

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Fig. 3

Overview of all mutations

1(A-C)	
GGTGTGTTTAATTATGAGACTGAGACCACCTCTGTTATCCCAGCAGCTCGACTGTTCAAG	60
G V F N Y E T E T T-P S V I P A A R L F K	20
9(A-G) 2(A-C) 2(A-C)	
GCCTTTATCCTTGATGGCGATAACCTCTTTCCAAAGGTTGCACCCCAAGCCATTAGCAGT	120
A F I L D-G G D N-T L F P K-Q V A P Q A I S S	40
3(GA-TC) 7(AA-TG) 4(G-C) 6(GA-TC)	
GTTGAAAACATTGAAGGAAATGAGGGCCCTGGAACCATTAAAGAAGATCAGCTTTCCCGAA	180
V E N I E-S G N-S G G P G T I K K-N I S F P E-S	60
5(CA-TG)	
GGCCTCCCTTTCAAGTACGTGAAGGACAGAGTTGATGAGGTGGACCACACAAACTTCAAA	240
G L P F K Y V K D R V D E V D H T-A N F K	80
TACAATTACAGCGTGATCGAGGGCGGTCCCATAGGCGACACATTGGAGAAGATCTCCAAC	
Y N Y S V I E G G P I G D T L E K I S N	100
10(GAG-CAC) 8(CCC-TGG)	
GAGATAAAGATAGTGGCAACCCCTGATGGAGGATCCATCTTGAAGATCAGCAACAAGTAC	360
E I K I V A T P-G D G G S I L K I S N K Y	120
CACACCAAAGGTGACCATGAGGTGAAGGCAGAGCAGGTTAAGGCAAGTAAAGAAATGGGC	
H T K G D H E V K A E Q V K A S K E M G	140
GAGACACTTTTGAGGGCCGTTGAGAGCTACCTCTTGGCACACTCCGATGCCCTAGAACTAA	
E T L L R A V E S Y L L A H S D A Y N stop	159

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FIG. 4

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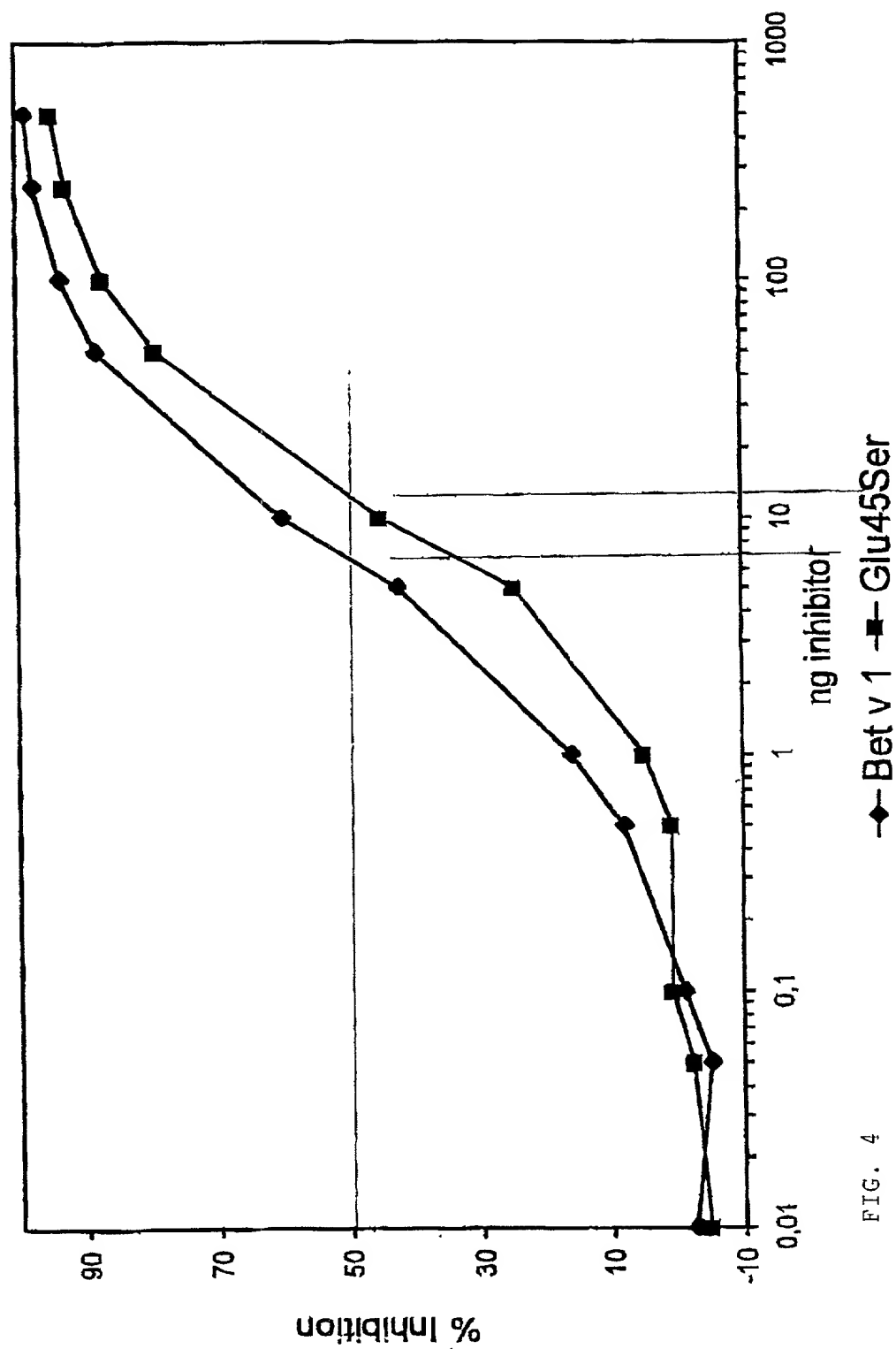


FIG. 4

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FIG. 5

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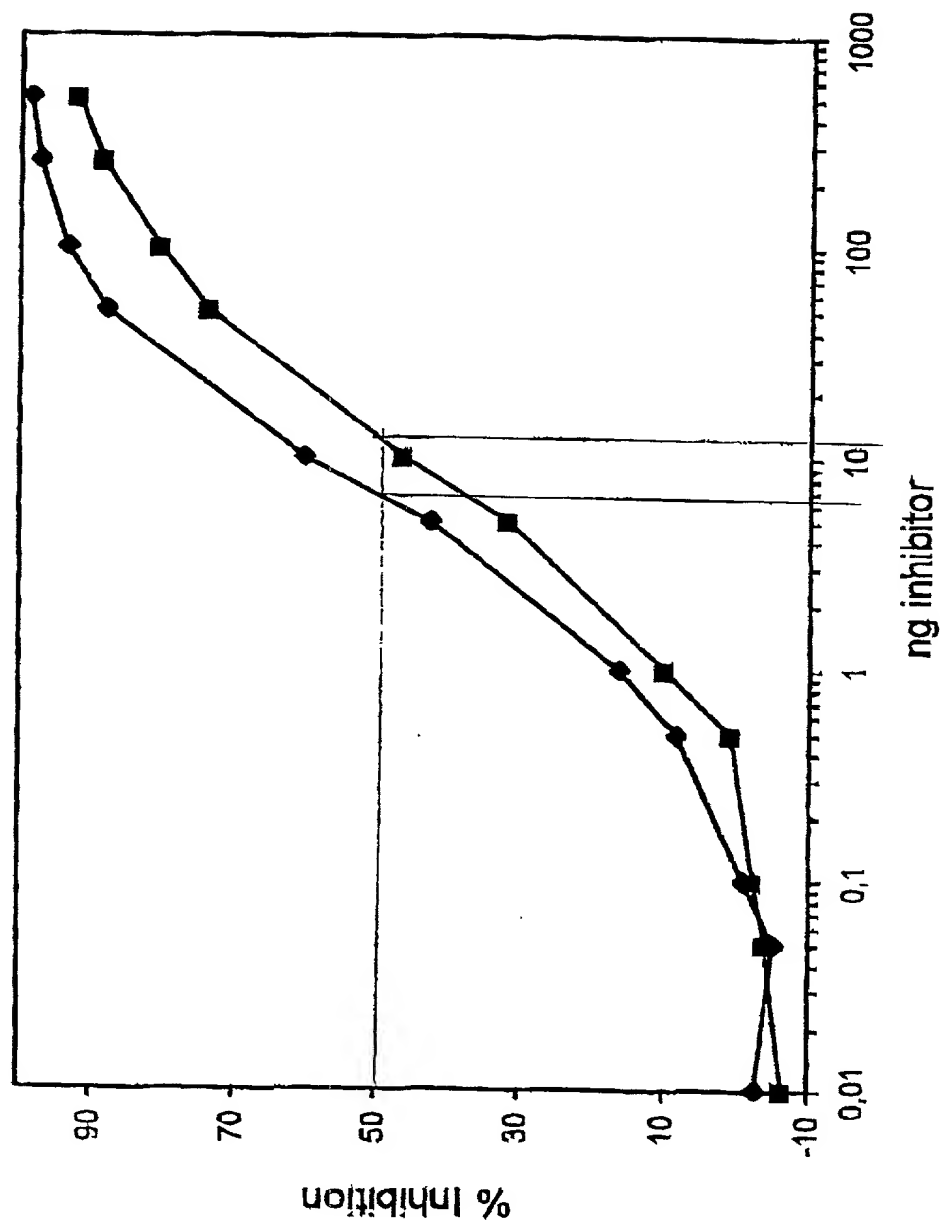


FIG. 5 ◆ Bet v 1 ■ Asn28Thr+Lys32Gln

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Fig. 6

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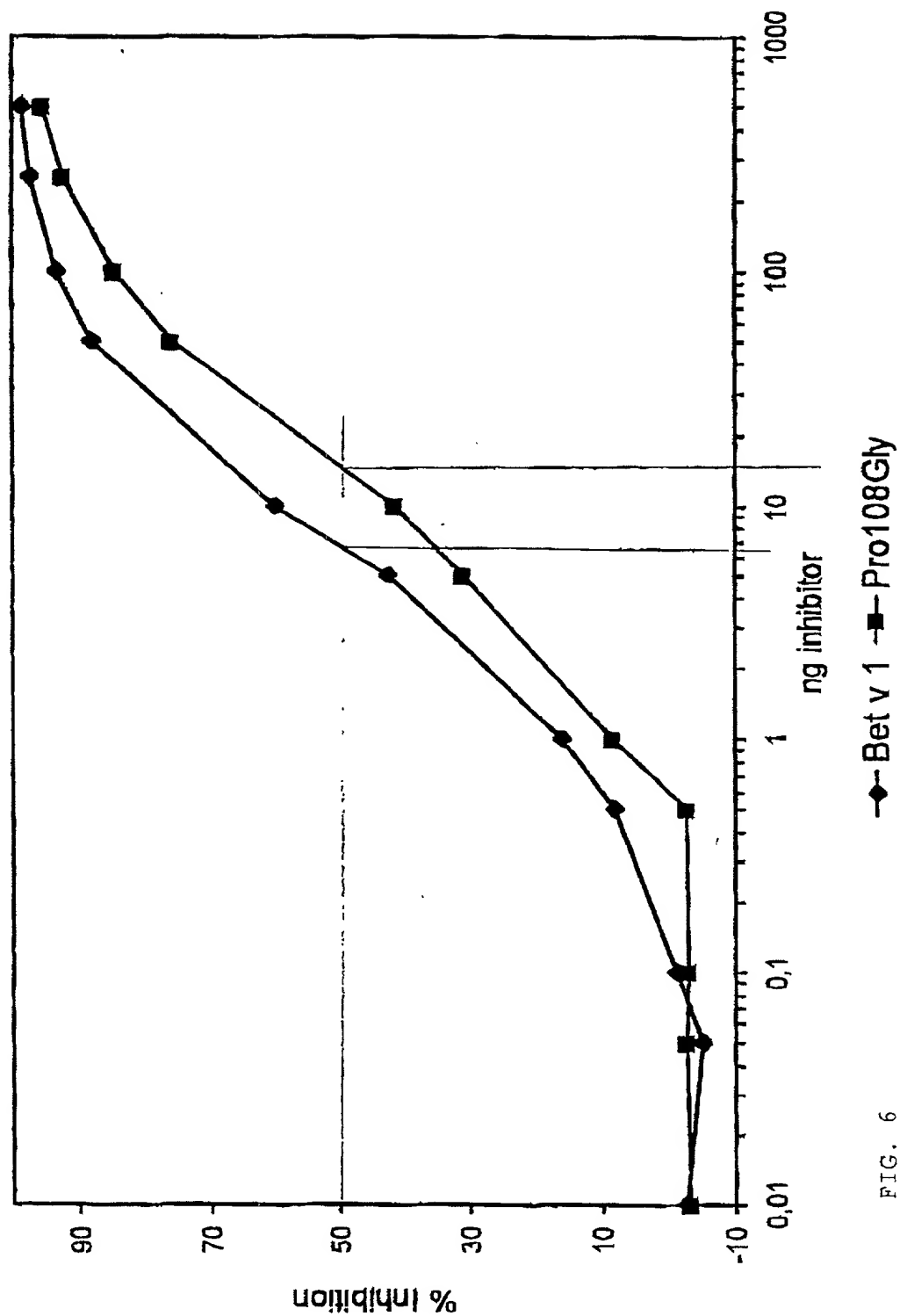


FIG. 6

Fig 7

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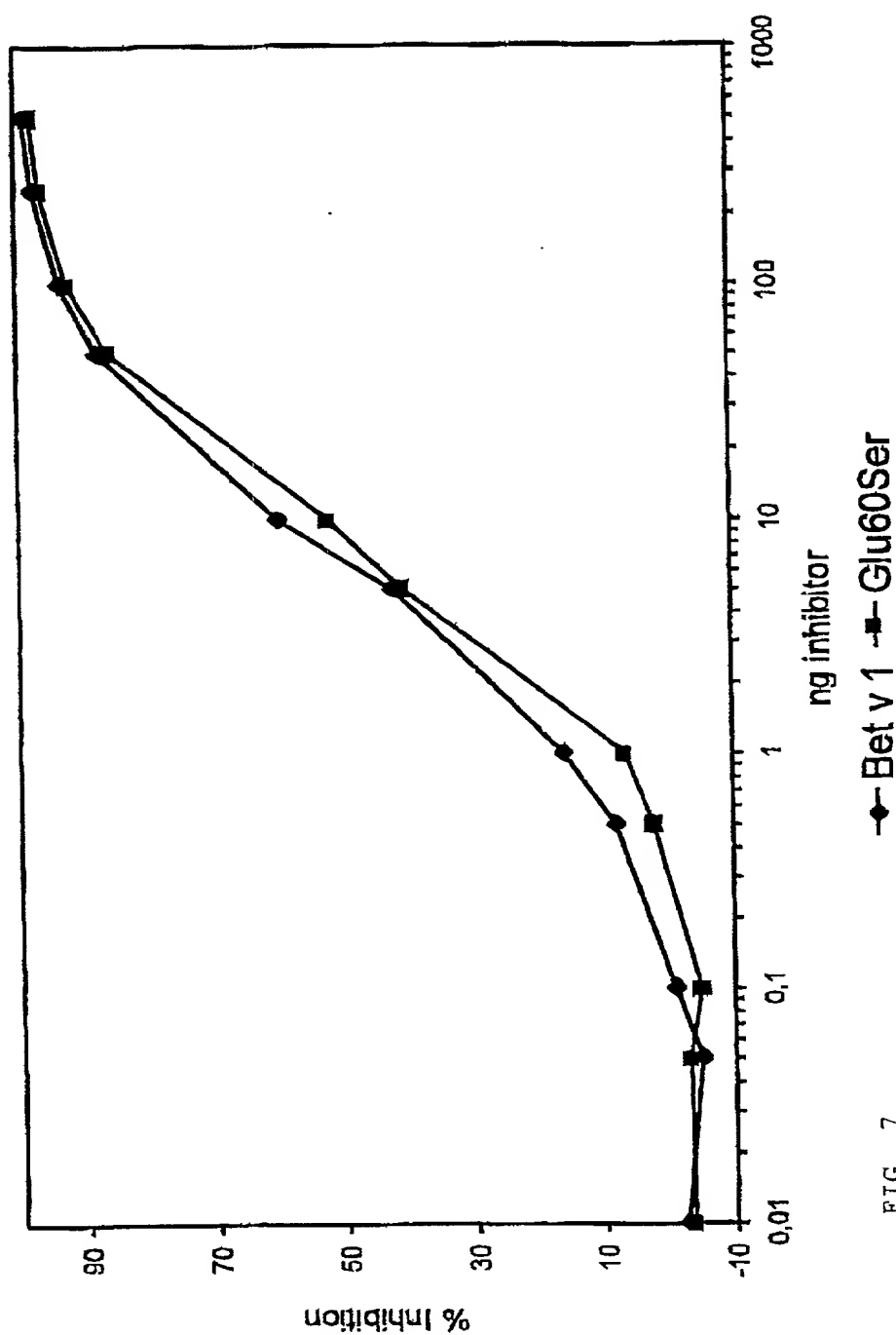
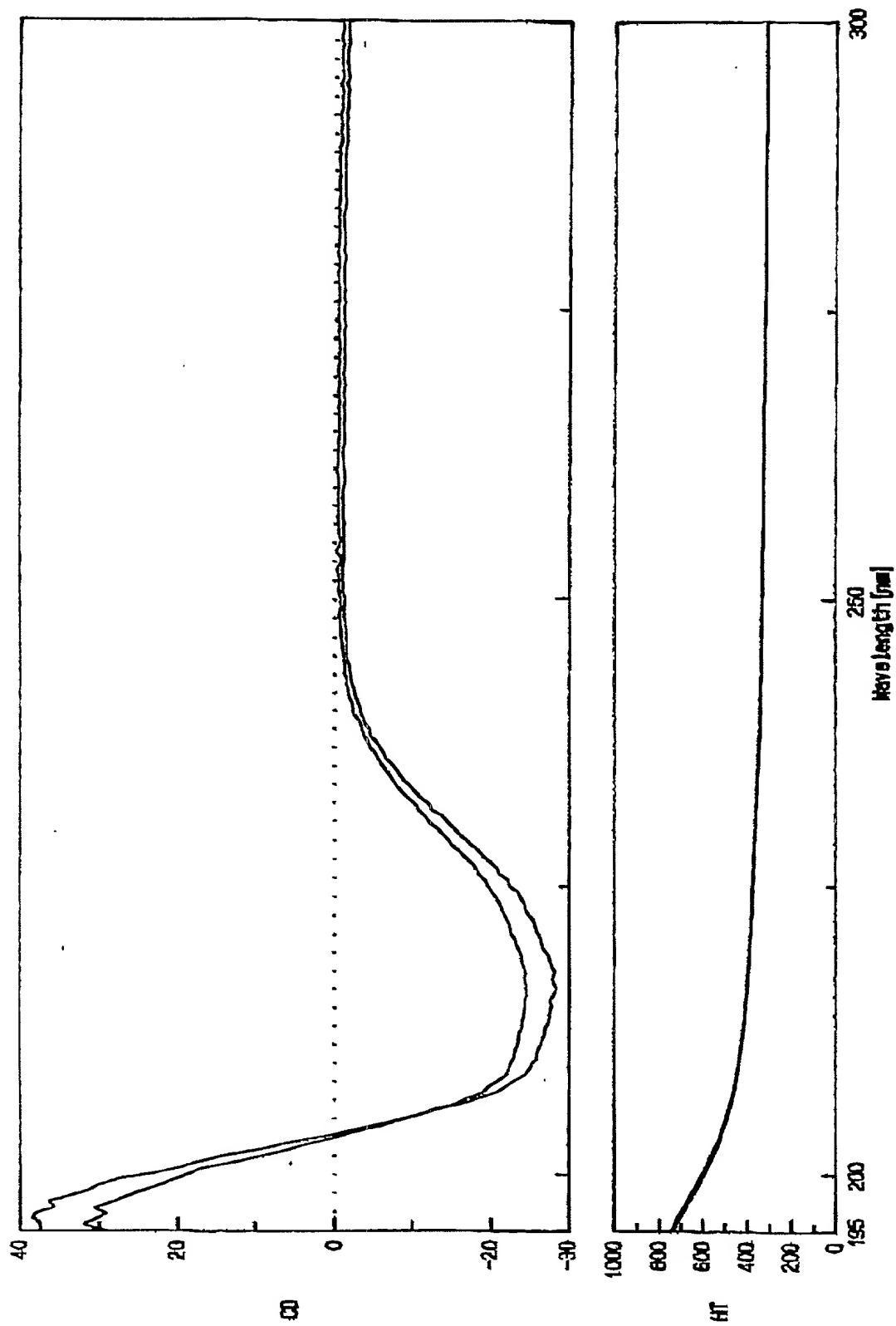


FIG. 7

Fig. 8

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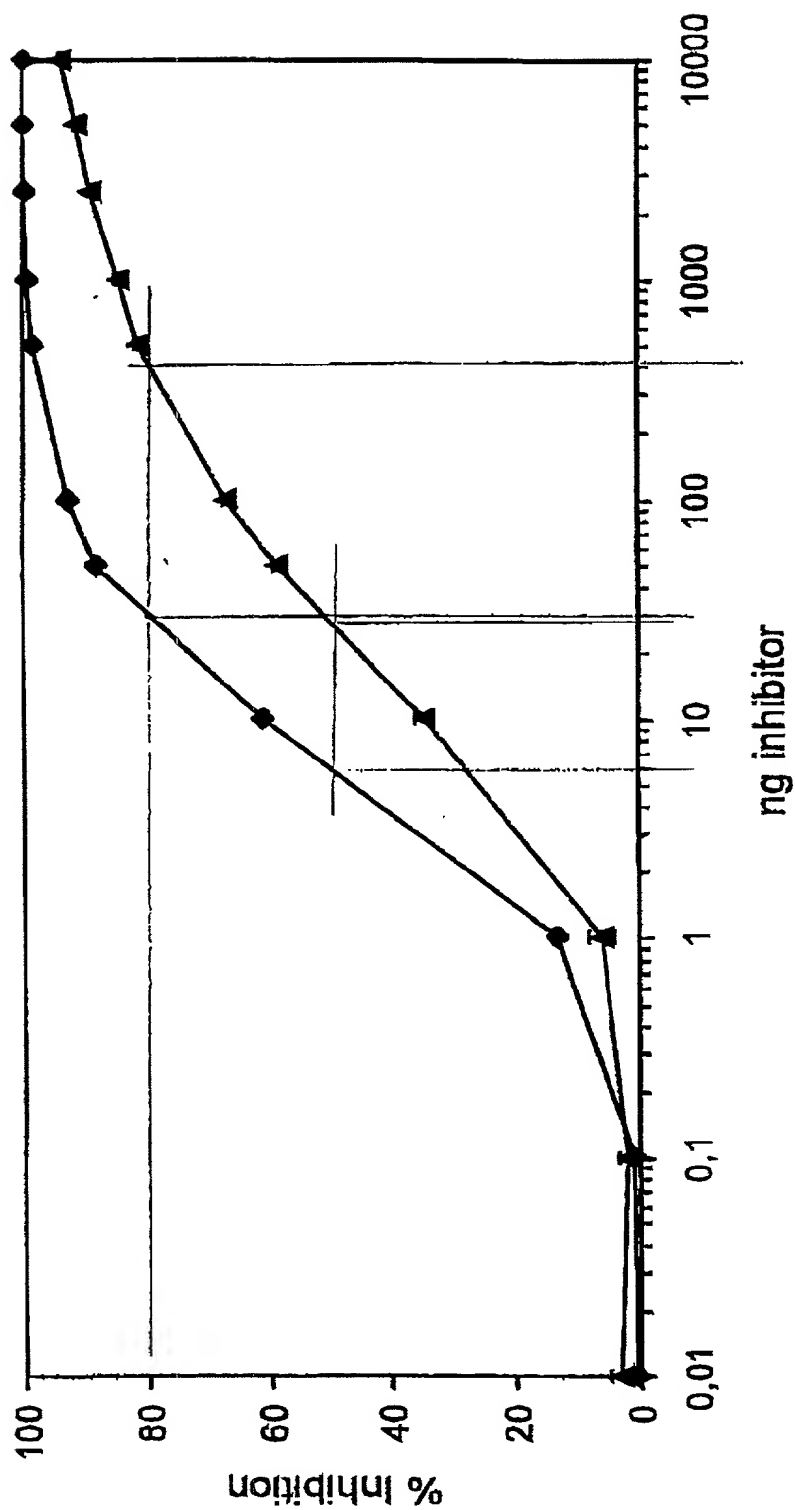


— Bety 2801
— Mutant 2535

FIG. 8

Fig. 9

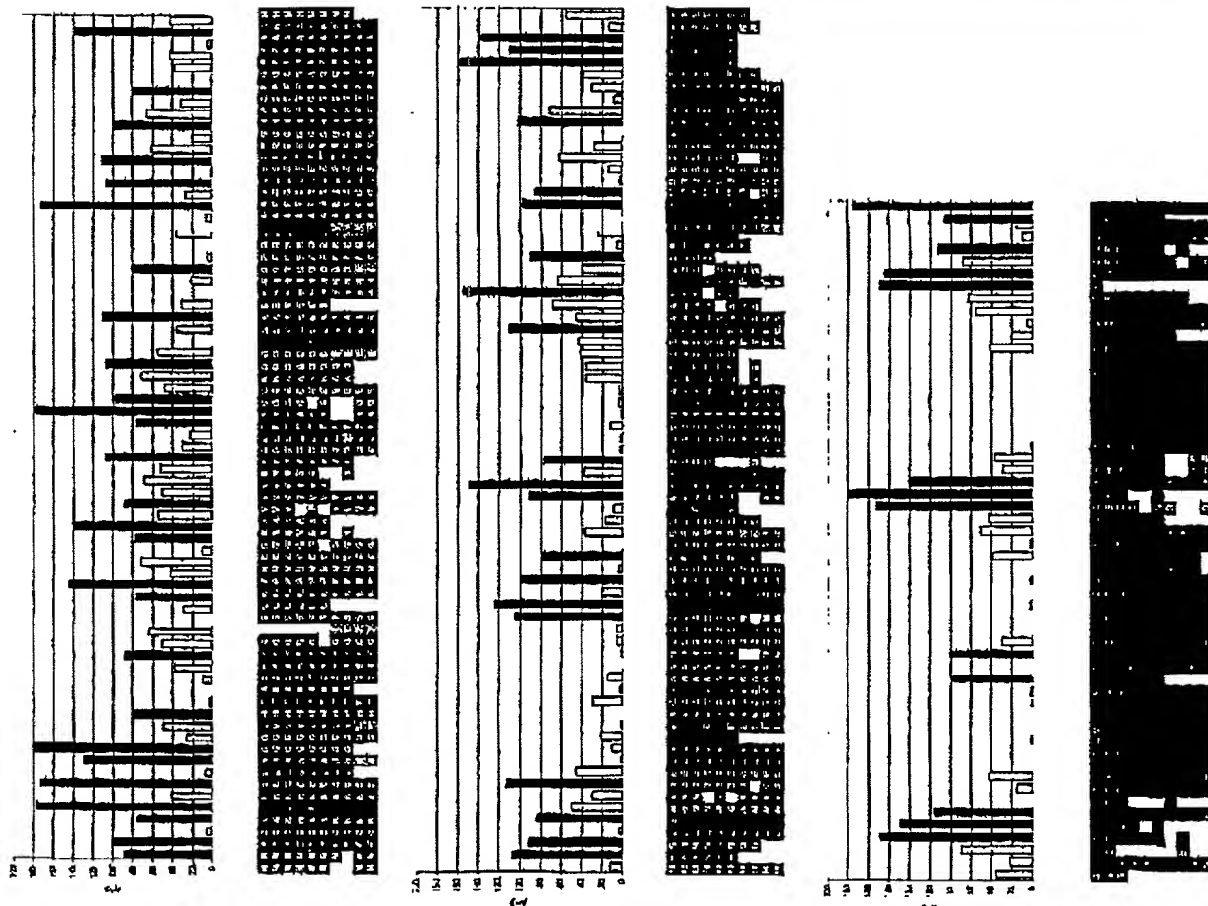
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—◆— Bet v 1 —▲— Glu45Ser, Pro108Gly, Asn28Thr+Lys32Gln.

FIG. 9

Conserved residues among Vespula antigen 5



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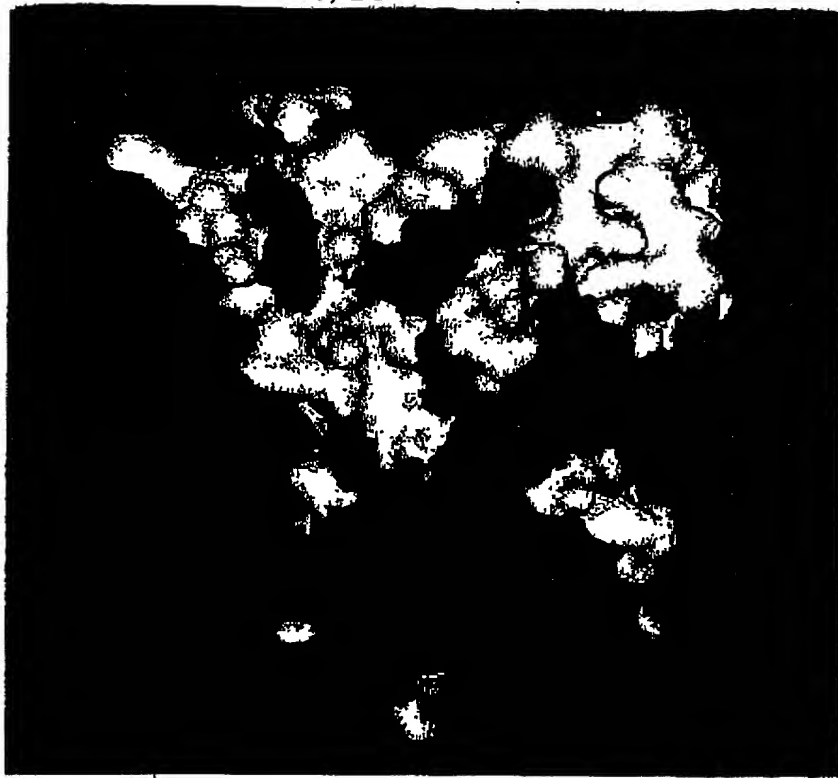


FIG. 10

Fig.11

Mutant-specific oligonucleotide primers used for Ves v 5 mutants.
Mutated nucleotides underlined.

Ves v 5 mutant 1 (K72A)

Ves v 5 sense	5'-	ACCACAGCCTCCAGCGAAGAATATGAAAAATTGGTATGGA	-3'
Ves v 5 non-sense	3'-	TGGTGTCGGAGGTGCTTCTTATACTTTTAAACCATACCT	-5'
sense primer	5'-	CCAGCG <u>GCT</u> AATATGAAAAAT	-3'
non-sense primer	3'-	GTCGGAGGTGCGCGA <u>TT</u> AATAC	-5'

Ves v 5 mutant 2 (Y96A)

Ves v 5 sense	5'-	GGCTAATCAATGTCAATATGGTCACGATACTTGCAGGGATG	-3'
Ves v 5 non-sense	3'-	CCGATTAGTTACAGTTATACCACTGCTATGAACGTCCCTAC	-5'
sense primer	5'-	TGTCAAG <u>CT</u> GGTCACGATACT	-3'
non-sense primer	3'-	TTAGTTACAGTTCAACCACTG	-5'

Fig. 12

Oligonucleotide primers for site directed mutagenesis of Ves v 5.

all sense 1: XhoI start, 38-mer:

EcoRI
 5'-CCGCTCGAGAAAAGAAACAATTATTGTAAATATAAATG
 L E K R N N Y C K I K
 Kex2 cleavage site amino terminus of Ves v 5

1	sense	1: K72As	21-mer	5'-CCAGCGGCTAATATGAAAAAT
1	non-sense	2: K72Aa	21-mer	5'-CATATTAGCCGCTGGAGGCTG
2	sense	3: Y96As	21-mer	5'-TGTCAAGCTGGTCACGATACT
2	non-sense	4: Y96Aa	21-mer	5'-GTGACCAGCTTGACATTGATT
all non-sense 7: CT-pPICZaA, 21-mer				5'-ATTCATCAGCTGCCGAGATAGG

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Fig. 13

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Overview of Ves v 5 mutations

1	AACAATTATTTGTAAAATAAAATGTTTGAAAGGAGGTGTCCATACTGCCTGCAAATATGGA	60
1	N N Y C K I K C L K G G V H T A C K Y G	20
61	AGTCTTAAACCGAATTGCGGTAATAAGGTAGTGGTATCCTATGGTCTAACGAAACAAGAG	120
21	S L K P N C G N K V V V S Y G L T K Q E	40
121	AAACAAGACATCTTAAAGGAGCACAAATGACTTTAGACAAAAAATTCACGAGGATTGGAG	180
41	K Q D I L K E H N D F R Q K I A R G L E	60
181	ACTAGAGGTAATCCTGGACCACAGCCTCCAGCGAAGAAATATGAAAAATTTGGTATGGAAC	240
61	T R G N P G P Q P P A K N M K N L V W N	80
241	GACGAGTTAGCTTATGTGCGCCCAAGTGTGGGCTAATCAATGTCAATATGGTCACGATACT	300
81	D E L A Y V A Q V W A N Q C Q Y G H D T	100
301	TGCAGGGATGTAGCAAAATATCAGGTGGACAAAACGTAGCCTTAACAGGTAGCACGGCT	360
101	C R D V A K Y Q V G Q N V A L T G S T A	120
361	GCTAAATACGATGATCCAGTTAAACTAGTTAAATGTGGGAAGATCAAGTGAAAGATTAT	420
121	A K Y D D P V K L V K M W E D E V K D Y	140
421	AATCCTAAGAAAAAGTTTTCGGGAAACGACTTTCTGAAAACCGGCCATTACACTCAAATG	480
141	N P K K K F S G N D F L K T G H Y T Q M	160
481	GTITGGGCTAACACCAAGGAAGTTGGTTGTGGAAGTATAAAATACATTCAAGAGAAATGG	540
161	V W A N T K E V G C G S I K Y I Q E K W	180
541	CACAAACATTACCTTGATGTAATTATGGACCCAGCGGAAACTTTAAGAATGAGGAACCTT	600
181	H K H Y L V C N Y G P S G N F K N E E L	200
601	TATCAAACAAAGTAA	612
201	Y Q T K stop	204

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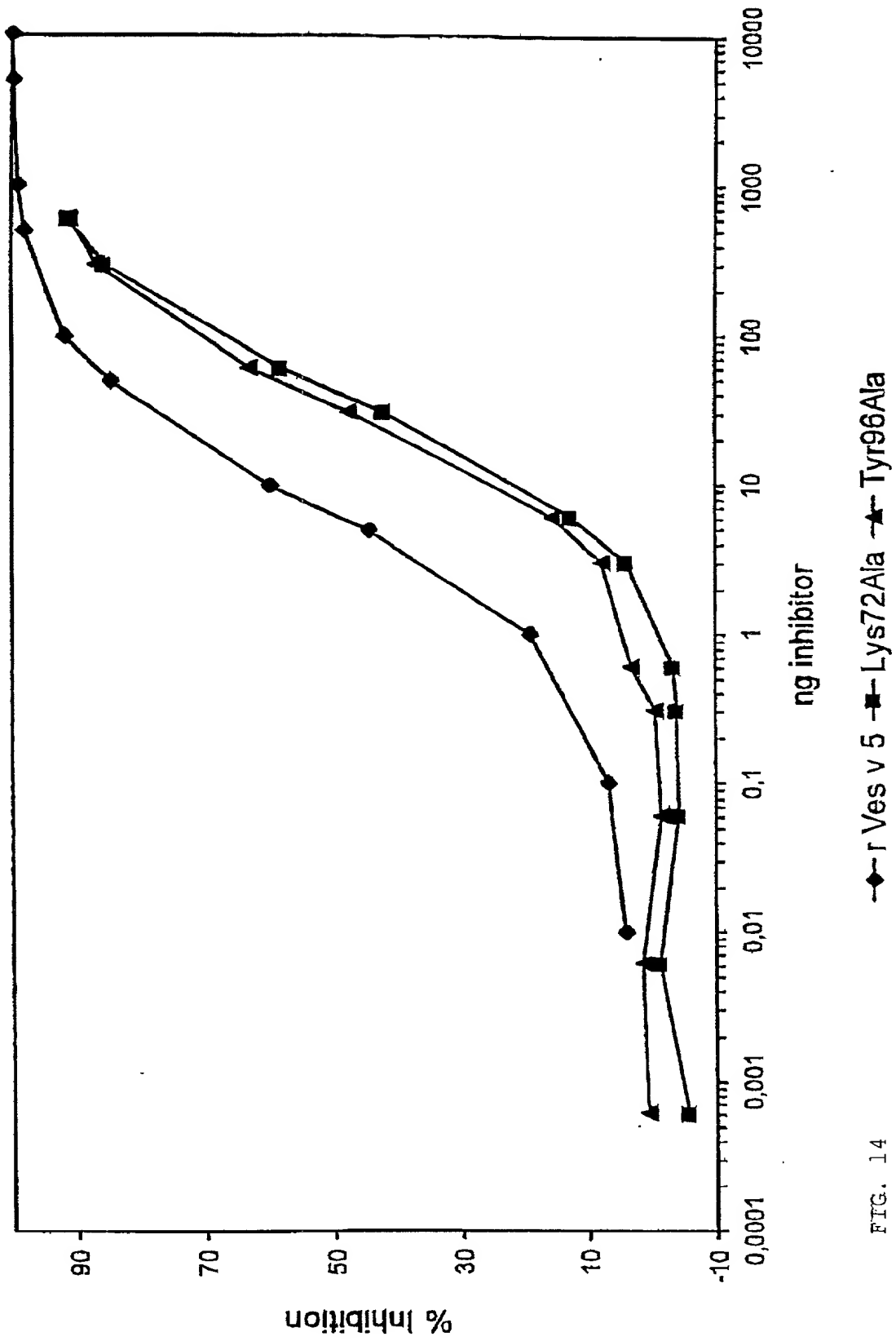


FIG. 14

**ALL FOREIGN APPLICATIONS, IF ANY, FILED PRIOR
TO THE APPLICATION(S) OF WHICH PRIORITY IS CLAIMED**

COUNTRY APPLICATION NO. DATE OF FILING

POWER OF ATTORNEY:

As a named inventor, I hereby appoint the following attorney(s) and/or agents(s) to prosecute this application and transact all business in the Patent and Trademark office connected therewith: Gordon D. Coplein #19,185, William F. Dudine, Jr. #20,569, Michael J. Sweedler #19,937, S. Peter Ludwig #25,351, Paul Fields #20,298, Marc S. Gross #19,614, Harold E. Wurst #22,183, Joseph B. Lerch #26,936, Melvin C. Garner #26,272, Ethan Horwitz #27,646, Beverly B. Goodwin #28,417, Adda C. Gogoris #29,714, Martin E. Goldstein #20,869, Bert J. Lewen #19,407, Henry Sternberg #22,408, Robert A. Green #28,301, Peter C. Schechter #31,662, Robert Schaffer #31,194, David R. Francescani #25,159, Robert C. Sullivan, Jr. #30,499, Ira J. Levy #35,587, Joseph R. Robinson #33,448

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CITY: STATE OR FOREIGN COUNTRY: COUNTRY OF CITIZENSHIP:
POST OFFICE ADDRESS: CITY: STATE OR COUNTRY: ZIP CODE:

I further declare that all statements made herein of my own knowledge are true and that all statements made on information and belief are believed to be true; and further that these statements were made with the knowledge that willful false statements and the like so made are punishable by fine or imprisonment, or both, under Section 1001 of Title 18 of the United States Code, and that such willful false statements may jeopardize the validity of the application or any patent issuing thereon.

SIGNATURE OF INVENTOR 1: _____ DATED: _____

SIGNATURE OF INVENTOR 2: _____ DATED: _____

SIGNATURE OF INVENTOR 3: _____ DATED: _____

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**DECLARATION
AND POWER OF ATTORNEY
Original Application**

As a below named inventor, I declare that the information given herein is true, that I believe that I am the original, first and sole inventor if only one name is listed at 1 below, or a joint inventor if plural inventors are named below, of the invention entitled:

NOVEL RECOMBINANT ALLERGENS

which is described and claimed in:

[X] the attached specification or [] the specification in application
Serial No. , filed
(for declaration not accompanying appl.)

that I do not know and do not believe that the same was ever known or used in the United States of America before my or our invention thereof or patented or described in any printed publication in any country before my or our invention thereof, or more than one year prior to this application, or in public use or on sale in the United States of America more than one year prior to this application, that the invention has not been patented or made the subject of an inventor's certificate issued before the date of this application in any country foreign to the United States of America on an application filed by me or my legal representatives or assigns more than twelve months prior to this application, that I acknowledge my duty to disclose information of which I am aware which is material to patentability in accordance with 37 CFR §1.56. I hereby state that I have reviewed and understand the contents of the above-identified specification, including the claims, as amended by any amendment referred to above. I hereby claim the priority benefits under 35 U.S.C. §119 of any application(s) for patent or inventor's certificate listed below. All foreign applications for patent or inventor's certificate on this invention filed by me or my legal representatives or assigns prior to the application(s) of which priority is claimed are also identified below.

PRIOR APPLICATION(S), IF ANY, OF WHICH PRIORITY IS CLAIMED

<u>COUNTRY</u>	<u>APPLICATION NO.</u>	<u>DATE OF FILING</u>
United States	60/078,371	March 18, 1998